

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 31, 2005, 17:35:30 ; Search time 77 Seconds
(without alignments)
3661.834 Million cell updates/sec

Title: US-10-509-307-1

Perfect score: 4055

Sequence: 1 MAPGTGSSAVNSCSQSL.....LQPKSQASKPAYGNSPYWTN 786

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 358729299 residues ;

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4055	100.0	786	7 ADP09771	Adp09771 Complete
2	3902	96.2	757	7 ADP09776	Adp09776 JNK3 huma
3	3083	76.0	597	4 AAM93397	Aam93397 Human pol
4	3083	76.0	597	8 ADL30961	Adl30961 Human pro
5	1536	37.9	363	3 RAY9361	Ray9361 Human PRO
6	1536	37.9	363	4 AAB66110	Aab66110 Protein o
7	1536	37.9	363	4 AAU29149	Aau29149 Human PRO
8	1536	37.9	363	6 ABU58525	Abu58525 Human PRO
9	1536	37.9	363	6 ABU8073	Abu8073 Novel hum
10	1536	37.9	363	6 ABU84388	Abu84388 Human sec
11	1536	37.9	363	6 ABR6262	Abr6262 Human sec
12	1536	37.9	363	6 ABR6562	Abr6562 Human sec
13	1536	37.9	363	6 ABU9592	Abu9592 Human sec
14	1536	37.9	363	6 ABU82831	Abu82831 Human PRO
15	1536	37.9	363	6 ABU89952	Abu89952 Novel hum
16	1536	37.9	363	6 ABR68201	Abr68201 Human sec
17	1536	37.9	363	6 ABU96254	Abu96254 Novel hum
18	1536	37.9	363	6 ABU92685	Abu92685 Human sec
19	1536	37.9	363	6 ABO08762	Abu08762 Human sec
20	1536	37.9	363	6 ABO02814	Abu02814 Human sec
21	1536	37.9	363	6 ABR74968	Abr74968 Human sec
22	1536	37.9	363	6 ABR94730	Abr94730 Human sec
23	1536	37.9	363	6 ABU85703	Abu85703 Human PRO
24	1536	37.9	363	6 ABU98863	Abu98863 Novel hum
25	1536	37.9	363	6 ABU98078	Abu98078 Novel hum

26	1536	37.9	363	6 ABU91784	Abu91784 Novel hum
27	1536	37.9	363	6 ABU89477	Abu89477 Human PRO
28	1536	37.9	363	6 ABU86318	Abu86318 Human sec
29	1536	37.9	363	6 ABU67531	Abu67531 Human sec
30	1536	37.9	363	6 ABU80559	Abu80559 Human PRO
31	1536	37.9	363	6 ABR99477	Abr99477 Human sec
32	1536	37.9	363	6 ABR98867	Abr98867 Human sec
33	1536	37.9	363	6 ABO16390	Abu16390 Human sec
34	1536	37.9	363	6 ABR92290	Abr92290 Human sec
35	1536	37.9	363	6 ABO18931	Abu18931 Human sec
36	1536	37.9	363	6 ABR78352	Abr78352 Human sec
37	1536	37.9	363	6 ABU85088	Abu85088 Novel hum
38	1536	37.9	363	6 ABO00227	Abu00227 Novel hum
39	1536	37.9	363	6 ABO11559	Abu11559 Human sec
40	1536	37.9	363	6 ABO02204	Abu02204 Human sec
41	1536	37.9	363	6 ABU88778	Abu88778 Novel hum
42	1536	37.9	363	6 ABU83473	Abu83473 Human sec
43	1536	37.9	363	6 ABO06274	Abu06274 Novel hum
44	1536	37.9	363	6 ABR59310	Abr59310 Human sec
45	1536	37.9	363	6 ABO09372	Abu09372 Human sec

ALIGNMENTS

RESULT 1

ADP09771
ID ADP09771 standard; protein; 786 AA.
AC ADP09771;
XX
DT 29-JUL-2004 (first entry)
XX
DE Complete human KIAA1491 protein sequence.
XX
KW c-Jun phosphorylation; c-Jun N-terminal kinase 3; Nootropic;
neuroprotective; Alzheimer's disease; apoptosis; BMAL1; PBPI; KIAA1491;
KIAA0596CT; JNK3.
XX
OS Homo sapiens.
XX
PN WO2003086462-A1.
XX
PD 23-OCT-2003.
XX
PF 31-MAR-2003; 2003WO-JP004120.
XX
PR 29-MAR-2002; 2002JP-00095291.
PR 29-MAR-2002; 2002JP-00095390.
PR 29-MAR-2002; 2002JP-00095442.
PR 29-MAR-2002; 2002JP-00095486.
PA (CELE-) CELESTAR LEXICO SCI INC.
PA (DAUC) DAIICHI PHARM CO LTD.
PI Doi H, Wada N, Nakajima H;
XX WPI; 2003-833621/77.
DR N-PSDB; ADP09777.
XX
PT Inhibitors of c-Jun phosphorylation including BMAL1, BPL1, KIAA1491,
KIAA0596 and their derivatives, for medical compositions and drugs for
treating neurodegenerative diseases e.g. Alzheimer's disease.
XX
PS Claim 1; SEQ ID NO 1; 139pp; Japanese.
XX
CC The present invention relates to inhibitors of c-Jun phosphorylation
contain as active ingredient 1 or more peptides that have a function of
interacting with c-Jun N-terminal kinase 3. Such peptides can inhibit the
phosphorylation or transcription activation of c-Jun, and can also
inhibit apoptosis of e.g. nerve cells. Proteins interacting with JNK3
were investigated in silico. Then, BMAL1, PBPI, KIAA1491 complete and
KIAA0596CT proteins were identified and their interaction with JNK3

CC confirmed. The present sequence represents the complete human KIAA1491
protein sequence.
XX
SQ Sequence 786 AA;
Query Match 100.0%; Score 4055; DB 7; Length 786;
Best Local Similarity 100.0%; Pred. No. 2.2e-236;
Matches 786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPGTSSSTAVNSCSQSSVSSVLSGSGFGLAPPKMANITSSQILDQLKAPSLGQFTTTPS 60
DB 1 MAPGTSSSTAVNSCSQSSVSSVLSGSGFGLAPPKMANITSSQILDQLKAPSLGQFTTTPS 60
QY 61 TQONSTSHPTTTSWDLKPTSSQSSVLSHLDKFSQPEPSVLSQSORQHQSOQAVTVPP 120
DB 61 TQONSTSHPTTTSWDLKPTSSQSSVLSHLDKFSQPEPSVLSQSORQHQSOQAVTVPP 120
QY 121 PGLSEPPQAKLRESTPGDSPSTVNWKLQLPSTTIENISVSHQPOPKHIKAKRIPPA 180
DB 121 PGLSEPPQAKLRESTPGDSPSTVNWKLQLPSTTIENISVSHQPOPKHIKAKRIPPA 180
QY 181 SKIPASAVEMPGSADVTGLNVQFGLFEGSEPSLSEFGSAPSENNOIPISLYSKSLSE 240
DB 181 SKIPASAVEMPGSADVTGLNVQFGLFEGSEPSLSEFGSAPSENNOIPISLYSKSLSE 240
QY 241 PLNTSLMTSAVQNSTYTTTSSVITSCSLTSSLSNAPVAMSSSYDQSSVHNRIPIQSPVS 300
DB 241 PLNTSLMTSAVQNSTYTTTSSVITSCSLTSSLSNAPVAMSSSYDQSSVHNRIPIQSPVS 300
QY 301 SSESAPGTIMNGHGGGRSQOTLPTKTTGPPSALPSVSSLPSTTCTALLPSTSOHTGDL 360
DB 301 SSESAPGTIMNGHGGGRSQOTLPTKTTGPPSALPSVSSLPSTTCTALLPSTSOHTGDL 360
QY 361 TSSPLSOLSSLSHQSSLSHAHALSSSTGHTHASVESASHOSSATFSTAATSVSSAS 420
DB 361 TSSPLSOLSSLSHQSSLSHAHALSSSTGHTHASVESASHOSSATFSTAATSVSSAS 420
QY 421 SGVSLSSMNTANSLCLGGTPASASSSSRAAPLVTSGKAPPNLPQGVPLLNQVILVGP 480
DB 421 SGVSLSSMNTANSLCLGGTPASASSSSRAAPLVTSGKAPPNLPQGVPLLNQVILVGP 480
QY 481 GGLLPAYPIYGYDELOMLQSLRPVDYIGIPPAAPTALASDRSLANNPYGCDVTKFGRGD 540
DB 481 GGLLPAYPIYGYDELOMLQSLRPVDYIGIPPAAPTALASDRSLANNPYGCDVTKFGRGD 540
QY 541 SASPAPATTPAQPOQSQSQTHTTAQPPFVNPALPPGYSTGLPYTGMPSAFQYGTMTFV 600
DB 541 SASPAPATTPAQPOQSQSQTHTTAQPPFVNPALPPGYSTGLPYTGMPSAFQYGTMTFV 600
QY 601 PPASAKQHGVLNSTPTPPFQOASQYGHGYSTGYDDLTQGTAAAGDYSKGGYAGSSQAPNK 660
DB 601 PPASAKQHGVLNSTPTPPFQOASQYGHGYSTGYDDLTQGTAAAGDYSKGGYAGSSQAPNK 660
QY 661 SAGSGPGKGVSVSSSTTGLPDMTGSVYNTQTTFKQGFHAGTPTPPFSLPSVLGSGPLAS 720
DB 661 SAGSGPGKGVSVSSSTTGLPDMTGSVYNTQTTFKQGFHAGTPTPPFSLPSVLGSGPLAS 720
QY 721 GAAPGYAPPPFHLIPAHQPHSOLLHLLPDAQSGSGQSQSPSSLOPKSQASKPAYGN 780
DB 721 GAAPGYAPPPFHLIPAHQPHSOLLHLLPDAQSGSGQSQSPSSLOPKSQASKPAYGN 780
QY 781 SPYWTN 786
DB 781 SPYWTN 786
RESULT 2
ADP09776
ID ADP09776 standard; protein; 757 AA.
XX
AC ADP09776;
XX
DT 29-JUL-2004 (first entry)

XX
DE
XX
KW
KW
KW
KW
XX
OS
XX
FN
XX
PD
XX
PF
XX
PR
XX
PR
XX
PR
XX
PA
XX
PI
XX
XX
DR
XX
PT
XX
PT
XX
PS
XX
XX
CC
CC
CC
CC
CC
CC
CC
CC
CC
XX
SQ
Query Match 96.2%; Score 3902; DB 7; Length 757;
Best Local Similarity 99.9%; Pred. No. 3.6e-227;
Matches 756; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 30 LAPPKMANITSSQILDQLKAPSLGQFTTTPSTQONSTSHPTTTSWDLKPPTSQSSVLSH 89
DB 1 LAPPKMANITSSQILDQLKAPSLGQFTTTPSTQONSTSHPTTTSWDLKPPTSQSSVLSH 60
QY 90 LDFKSPSPVLSQSORQHQSOQAVTVPPGLESPFQAKLRESTPGDSPSTVNWKLQ 149
DB 61 LDFKSPSPVLSQSORQHQSOQAVTVPPGLESPFQAKLRESTPGDSPSTVNWKLQ 120
QY 150 LPSTTIENISVSHQPOPKHIKAKRIPPAKIPASAVEMPGSADVTGLNVQFGLFEG 209
DB 121 LPSTTIENISVSHQPOPKHIKAKRIPPAKIPASAVEMPGSADVTGLNVQFGLFEG 180
QY 210 SEPSLSEFGSAPSENNOIPISLYSKSLSEPLNTSLMTSAVQNSTYTTTSSVITSCSLTS 269
DB 181 SEPSLSEFGSAPSENNOIPISLYSKSLSEPLNTSLMTSAVQNSTYTTTSSVITSCSLTS 240
QY 270 SSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSESAPGTIMNGHGGGRSQOTLPTKTTG 329
DB 241 SSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSESAPGTIMNGHGGGRSQOTLPTKTTG 300
QY 330 PPSALPSVSSLPSTTCTALLPSTSOHTGDLTSSPLSOLSSLSHQSSLSHAHALSSST 389
DB 301 PPSALPSVSSLPSTTCTALLPSTSOHTGDLTSSPLSOLSSLSHQSSLSHAHALSSST 360

JNK3 human KIAA1491 protein.
c-Jun phosphorylation; c-Jun N-terminal kinase 3; Nootropic;
neuroprotective; Alzheimer's disease; apoptosis; BMAL1; PP1; KIAA1491;
KIAA0596CT; JNK3.

Homio sapiens.
WO2003086462-A1.
23-OCT-2003.

31-MAR-2003; 2003WO-JP004120.
29-MAR-2002; 2002JP-00095291.
29-MAR-2002; 2002JP-00095390.
29-MAR-2002; 2002JP-00095442.
29-MAR-2002; 2002JP-00095486.
(CELE-) CELESTAR LEXICO SCI INC.
(DAUC) DALICHI PHARM CO LTD.

Doi H, Wada N, Nakajima H;
WPI; 2003-833621/77.

Inhibitors of c-Jun phosphorylation including BMAL1, BPL1, KIAA1491,
KIAA0596 and their derivatives, for medical compositions and drugs for
treating neurodegenerative diseases e.g. Alzheimer's disease.

Claim 1; SEQ ID NO 6; 139pp; Japanese.

The present invention relates to inhibitors of c-Jun phosphorylation
contain as active ingredient 1 or more peptides that have a function of
interacting with c-Jun N-terminal kinase 3. Such peptides can inhibit the
phosphorylation or transcription activation of c-Jun, and can also
inhibit apoptosis of e.g. nerve cells. Proteins interacting with JNK3
were investigated in silico. Then, BMAL1, PP1, KIAA1491 complete and
KIAA0596CT proteins were identified and their interaction with JNK3
confirmed. The present sequence represents the complete human JNK3
KIAA1491 protein sequence.

Sequence 757 AA;

QY 390 SHTHASVESASHOSSATFSTAATSVSASSGVSLSMMTANSLCLGGTPASASSSS 449
DB 361 SHTHASVESASHOSSATFSTAATSVSASSGVSLSMMTANSLCLGGTPASASSSS 420
QY 450 RAAPLVTSKAPPNLPQGVPPHLLHNOYLVGPGILLPAYPIYGYDELMQLQSLPVDYGI 509
DB 421 RAAPLVTSKAPPNLPQGVPPHLLHNOYLVGPGILLPAYPIYGYDELMQLQSLPVDYGI 480
QY 510 PFAAPTALASDRSLANNPYGCDVTKFGKGDSPAPATTPAQPOQSQSQTHTTAQPFV 569
DB 481 PFAAPTALASDRSLANNPYGCDVTKFGKGDSPAPATTPAQPOQSQSQTHTTAQPFV 540
QY 570 NPALPPGVSYTGCLPYTTCMPAFQYGTMTFPPASAKOHVNLSTPTPPFQOASGYGQH 629
DB 541 NPALPPGVSYTGCLPYTTCMPAFQYGTMTFPPASAKOHVNLSTPTPPFQOASGYGQH 600
QY 630 YSTGYDDLTOGTAAGDYSGKGVAGSQAPNKSAGSGPGKGVSVSSTTGLPDMTGSVYNK 689
DB 601 YSTGYDDLTOGTAAGDYSGKGVAGSQAPNKSAGSGPGKGVSVSSTTGLPDMTGSVYNK 660
QY 690 TOTFDKQGFHAGTTPPFPSLVLSGTGPLASGAAPGYAPPPFLHILPAHQPHSQQLLHH 749
DB 661 TOTFDKQGFHAGTTPPFPSLVLSGTGPLASGAAPGYAPPPFLHILPAHQPHSQQLLHH 720
QY 750 LPQDAQSGSGQRSPSSLOPKSQASKPAYGNSPYWTN 786
DB 721 LPQDAQSGSGQRSPSSLOPKSQASKPAYGNSPYWTN 757

RESULT 3

ADL30961
ID ANM93397 standard; protein; 597 AA.
AC ANM93397;
XX
XX
DT 06-NOV-2001 (first entry)
XX
XX Human polypeptide, SEQ ID NO: 2994.
XX
XX Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
XX Homo sapiens.
XX
XX EPI130094-A2.
XX
XX
XX 05-SEP-2001.
XX
XX 07-JUL-2000; 2000EP-00114089.
XX
XX 08-JUL-1999; 99JP-00194486.
XX
XX 11-JAN-2000; 2000JP-00118774.
XX
XX 02-MAY-2000; 2000JP-00183765.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX
XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
XX WPI; 2001-524255/58.
XX
XX N-PSDB; AAK94318.

830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.

Claim 8; SEQ ID NO 2994; 1380pp + Sequence Listing; English.

The invention relates to primers for synthesizing full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesizing the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers

CC enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
XX
SQ Sequence 597 AA;

Query Match 76.0%; Score 3083; DB 4; Length 597;
Best Local Similarity 99.7%; Pred. No. 8.2e-178;
Matches 595; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 190 MPGADVTGLNVQFALFPGSEPSLSFGSAPSSNSNQIPISLYSKLSPLNTSLMT 249
DB 1 MPGADVTGLNVQFALFPGSEPSLSFGSAPSSNSNQIPISLYSKLSPLNTSLMT 60
QY 250 SAVONSTYTTSVITSCSLTSSLSNASPVMSSSYDQSSVHNRIPIYQSPVSSSESAPGTI 309
DB 61 SAVONSTYTTSVITSCSLTSSLSNASPVMSSSYDQSSVHNRIPIYQSPVSSSESAPGTI 120
QY 310 MNGHGGGRSQOTLDTPTKTTGPPSALPSVSSLPSTTCTALLPSTSQHTGDLTSSPLSOLS 369
DB 121 MNGHGGGRSQOTLDTPTKTTGPPSALPSVSSLPSTTCTALLPSTSQHTGDLTSSPLSOLS 180
QY 370 SSLSSHQSLSAHAALSSSTSHTHASVESASHOSSATFTAAATSVSSASGVSLSSSM 429
DB 181 SSLSSHQSLSAHAALSSSTSHTHASVESASHOSSATFTAAATSVSSASGVSLSSSM 240
QY 430 NTANSLCIGGTPASASSSSRAAPLVTSKAPPNLPQGVPPHLLHNOYLVGPGILLPAYPI 489
DB 241 NTANSLCIGGTPASASSSSRAAPLVTSKAPPNLPQGVPPHLLHNOYLVGPGILLPAYPI 300
QY 490 YGYDELMQLQSLPVDYGIIPFAAPTALASDRSLANNPYGCDVTKFGKGDSPAPATTPATT 549
DB 301 YGYDELMQLQSLPVDYGIIPFAAPTALASDRSLANNPYGCDVTKFGKGDSPAPATTPATT 360
QY 550 PAQPOQSQSOTHTTAQPFVNPALPPGYSYTGLPYTTCMPSAFOYGTMTFPPASAKOHG 609
DB 361 PAQPOQSQSOTHTTAQPFVNPALPPGYSYTGLPYTTCMPSAFOYGTMTFPPASAKOHG 420
QY 610 VNLSTPTPPFQOASGYGQHGYSTGYDDLTOGTAAGDYSGKGVAGSQAPNKSAGSGPGKG 669
DB 421 VNLSTPTPPFQOASGYGQHGYSTGYDDLTOGTAAGDYSGKGVAGSQAPNKSAGSGPGKG 480
QY 670 VSVSSSTTGLPDMTGSVYNKTOTFDKQGFHAGTTPPFPSLVLSGTGPLASGAAPGYAPP 729
DB 481 VSVSSSTTGLPDMTGSVYNKTOTFDKQGFHAGTTPPFPSLVLSGTGPLASGAAPGYAPP 540
QY 730 PFLHILPAHQPHSQQLLHHLPQDAQSGSGQRSPSSLOPKSQASKPAYGNSPYWTN 786
DB 541 PFLHILPAHQPHSQQLLHHLPQDAQSGSGQRSPSSLOPKSQASKPAYGNSPYWTN 597

RESULT 4

ADL30961
ID ADL30961 standard; protein; 597 AA.
AC ADL30961;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human protein encoded by a full length cDNA clone SeqID 2994.
XX
XX human; medicine; signal transduction; glycoprotein; transcription;
XX
XX oligo-capping method.
XX
XX Homo sapiens.
XX
XX EPI396543-A2.
XX
XX 10-MAR-2004.
XX
XX 07-JUL-2000; 2003EP-00025638.

541 PFLHILPAHQPHSOLLHHHLPODAQSGSQRSQPSLQFKSQASKPAYGNSPYWTN 597

XX 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183865.
PR 07-JUL-2000; 2000JP-00114089.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX Ota T, Nishikawa T, Isogai T, Hayaashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2004-204755/20.
DR N-PSDB; ADL30960.
XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full
PT length human cDNAs.
XX Example 1; SEQ ID NO 2994; 1340pp; English.
XX This invention relates to a novel primers useful for synthesizing full
CC length cDNA molecules that encode human proteins. Specifically, it refers
CC to secretory or membrane proteins that are potential therapeutic agents/
CC target molecules in the field of medicine, and in particular genes
CC encoding proteins that are associated with signal transduction,
CC glycoproteins and transcription. The present invention describes a method
CC for efficiently cloning a full length human cDNA from both the 5' and 3'
CC ends using the oligo-capping method. This polypeptide sequence is a full
CC length human protein of the invention.
XX SQ Sequence 597 AA;
Query Match 76.0%; Score 3083; DB 8; Length 597;
Best Local Similarity 99.7%; Pred. No. 8.2e-178;
Matches 595; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 190 MFGADVTGLNVQGALEFGEPSLSEFGAPSENENQIPISLYSKSLSEPLNTLSMT 249
DB 1 MFGADVTGLNVQGALEFGEPSLSEFGAPSENENQIPISLYSKSLSEPLNTLSMT 60
QY 250 SAVQNSTYTTTSVITSCSLTSSLSNASFVAMSSYDQSSVHNRIPIQSPVSSSESAPGTI 309
DB 61 SAVQNSTYTTTSVITSCSLTSSLSNASFVAMSSYDQSSVHNRIPIQSPVSSSESAPGTI 120
QY 310 MNGHGGGRSQOQLDTPKTTGPPSALPVSSLSPTSTCTALLPSTSOHTGDLTSSPLSOLS 369
DB 121 MNGHGGGRSQOQLDTPKTTGPPSALPVSSLSPTSTCTALLPSTSOHTGDLTSSPLSOLS 180
QY 370 SSSLSSHQSLSAHAALSSSTGTHASVESASHQSSTATFSTAATSVSSASSSGVSLSSSM 429
DB 181 SSSLSSHQSLSAHAALSSSTGTHASVESASHQSSTATFSTAATSVSSASSSGVSLSSSM 240
QY 430 NTANSLCLGGTPASASSSSSRAAPLVTSGKAPPNLPQGVPPLLHNOYLVGPGLLPAYPI 489
DB 241 NTANSLCLGGTPASASSSSSRAAPLVTSGKAPPNLPQGVPPLLHNOYLVGPGLLPAYPI 300
QY 490 YGYDELOMLQSLPVDYVYIGIFPAAPTALASRDRLANNPYDGVTKFGRGDSASPAATT 549
DB 301 YGYDELOMLQSLPVDYVYIGIFPAAPTALASRDRLANNPYDGVTKFGRGDSASPAATT 360
QY 550 PAQPOQSQSQTHTTAQOQFVNPALPPGYSTGLPYTGMPSAFQYGTMTFVPPASAKQHG 609
DB 361 PAQPOQSQSQTHTTAQOQFVNPALPPGYSTGLPYTGMPSAFQYGTMTFVPPASAKQHG 420
QY 610 VNLSTPTPPFQASQGHGYSTGYDDLTQGTAAQDYSKGGYAGSSQAPNKSAGSGPKG 669
DB 421 VNLSTPTPPFQASQGHGYSTGYDDLTQGTAAQDYSKGGYAGSSQAPNKSAGSGPKG 480
QY 670 VSVSSSTGLPDMTGSVYKNTOTFDKQGFHAGTTPPFSVLPSVLGSGTGLASGAAPGYAPP 729
DB 481 VSVSSSTGLPDMTGSVYKNTOTFDKQGFHAGTTPPFSVLPSVLGSGTGLASGAAPGYAPP 540
QY 730 PFLHILPAHQPHSOLLHHHLPODAQSGSQRSQPSLQFKSQASKPAYGNSPYWTN 786

Db 541 PFLHILPAHQPHSOLLHHHLPODAQSGSQRSQPSLQFKSQASKPAYGNSPYWTN 597
RESULT 5
AAY99361
ID AAY99361 standard; protein; 363 AA.
XX AAY99361;
AC AAY99361;
XX 08-AUG-2000 (first entry)
XX Human PRO1197 (UNQ610) amino acid sequence SEQ ID NO:72.
XX Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX Homo sapiens.
XX WO200012708-A2.
XX 09-MAR-2000.
PF 01-SEP-1999; 99WO-US020111.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 02-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101479P.
PR 23-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.

[illegible]

PF	18-FEB-2000; 2000WO-US004342.	DT	18-DEC-2001 (first entry)
XX		XX	Human PRO polypeptide sequence #126.
PR	23-JUN-1999; 99US-0141037P.	DE	
PR	20-JUL-1999; 99US-0144758P.	XX	PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
PR	26-JUL-1999; 99US-0145698P.	KW	dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
PR	01-SEP-1999; 99WO-US020111.	KW	blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
PR	29-OCT-1999; 99US-0162506P.	KW	adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
PR	30-NOV-1999; 99WO-US028313.	XX	
PR	02-DEC-1999; 99WO-US028551.	OS	Homo sapiens.
PR	16-DEC-1999; 99WO-US030095.	XX	
PR	05-JAN-2000; 2000WO-US000219.	FN	WO200168848-A2.
PR	06-JAN-2000; 2000WO-US000376.	XX	
XX		XX	20-SEP-2001.
PA	(GETH) GENENTECH INC.	PD	
XX		XX	28-FEB-2001; 2001WO-US006520.
PI	Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;	PF	
PI	Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;	XX	01-MAR-2000; 2000WO-US005601.
PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;	PR	02-MAR-2000; 2000WO-US005841.
PI	Williams PM, Wood WI;	PR	03-MAR-2000; 2000US-0187202P.
XX		PR	06-MAR-2000; 2000US-0186968P.
XX	WPI; 2001-071395/08.	PR	14-MAR-2000; 2000US-0189320P.
DR		PR	14-MAR-2000; 2000US-0189328P.
XX		PR	15-MAR-2000; 2000WO-US006884.
XX	Secreted and transmembrane proteins and nucleic acids designated PRO,	PR	21-MAR-2000; 2000US-0190828P.
PT	useful as hybridization probes, in chromosome and gene mapping and gene	PR	21-MAR-2000; 2000US-0191007P.
PT	therapy.	PR	21-MAR-2000; 2000US-0191048P.
XX		PR	21-MAR-2000; 2000US-0191314P.
PS	Claim 1; Fig 44; 787pp; English.	PR	28-MAR-2000; 2000US-0192655P.
XX		PR	29-MAR-2000; 2000US-0193032P.
CC	The present invention relates to secreted and transmembrane proteins.	PR	29-MAR-2000; 2000US-0193053P.
CC	These proteins and the DNA encoding them may be used as hybridization	PR	30-MAR-2000; 2000WO-US008439.
CC	probes, in chromosome and gene mapping and in the generation of anti-	PR	04-APR-2000; 2000US-0194449P.
CC	sense RNA and DNA. They may also be used to generate either for	PR	04-APR-2000; 2000US-0194647P.
CC	transgenic animals or knockout animals which are in turn useful for	PR	11-APR-2000; 2000US-0195975P.
CC	development and screening of therapeutically useful reagents. The nucleic	PR	11-APR-2000; 2000US-0196000P.
CC	acids may also be used in gene therapy	PR	11-APR-2000; 2000US-0196187P.
XX		PR	11-APR-2000; 2000US-0196690P.
XX	Sequence 363 AA;	PR	11-APR-2000; 2000US-0196820P.
SQL		PR	18-APR-2000; 2000US-0198121P.
	Query Match 37.9%; Score 1536; DB 4; Length 363;	PR	18-APR-2000; 2000US-0198585P.
	Best Local Similarity 96.2%; Pred. No. 1.3e-84;	PR	25-APR-2000; 2000US-0199397P.
	Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;	PR	25-APR-2000; 2000US-0199550P.
QY	7 SSTAIVSCS--PQSLSSVLGSGFGLAPPKMANITSSQILDQLKAPSLGQFTTTPSTQON 64	PR	25-APR-2000; 2000US-0199654P.
DB	9 NSVLIRICSFPLKSSVLGSGFGLAPPKMANITSSQILDQLKAPSLGQFTTTPSTQON 68	PR	03-MAY-2000; 2000US-0201516P.
QY	65 STSHPTTTTMDLKPTTSQSSVLSHLDPKSQPEPSPVLSQLSQRQHQSOAVTVPPPGLE 124	PR	17-MAY-2000; 2000WO-US013705.
DB	69 STSHPTTTTMDLKPTTSQSSVLSHLDPKSQPEPSPVLSQLSQRQHQSOAVTVPPPGLE 128	PR	22-MAY-2000; 2000WO-US014041.
QY	125 SPFSQAKLRESTPGDSPSTVKNLQLPSTTTIENISVSVHQPPKHILAKRIRPPASKIP 184	PR	02-JUN-2000; 2000WO-US015264.
DB	129 SPFSQAKLRESTPGDSPSTVKNLQLPSTTTIENISVSVHQPPKHILAKRIRPPASKIP 188	PR	05-JUN-2000; 2000US-0203832P.
QY	185 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSFEGSAPSENSNQIPISLSKSLSEPLNT 244	PR	28-JUL-2000; 2000WO-US020710.
DB	189 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSFEGSAPSENSNQIPISLSKSLSEPLNT 248	PR	22-AUG-2000; 2000US-00644848.
QY	245 SLSMTSAVQNSTYTTSTVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 304	PR	24-AUG-2000; 2000WO-US023328.
DB	249 SLSMTSAVQNSTYTTSTVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 308	PR	08-NOV-2000; 2000WO-US030952.
QY	305 APGTIMNGHGGRSQOTLDT 324	PR	01-DEC-2000; 2000WO-US032678.
DB	309 APGTIMNGHGGRSQOTLDS 328	PR	20-DEC-2000; 2000WO-US034956.
RESULT 7		XX	(GETH) GENENTECH INC.
AAU29149		XX	Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
ID AAU29149	standard; protein; 363 AA.	PI	Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX		XX	WPI; 2001-602746/68.
XX		DR	N-PSDB; AAS46050.
XX		XX	Novel nucleic acids encoding PRO polypeptides, used to diagnose the
		PT	presence of tumors, such as prostate and breast tumors, in mammals and to
		PT	screen for modulators of the compounds.
		XX	Claim 11; Fig 252; 774pp; English.
		PS	Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
		CC	The PRO polypeptides and their associated nucleic acids can be used to

RESULT 8
ABU58525
ID ABU58525 standard; protein; 363 AA.
XX
XX AC AC
XX ABU58525;
XX
XX DT 15-APR-2003 (first entry)
XX
XX DE Human PRO polypeptide #126.
XX
XX Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
XX OS Homo sapiens.
XX
XX PN US2003027272-A1.
XX
XX PD 06-FEB-2003.
XX
XX PF 21-JUN-2002; 2002US-00176492.
XX
XX PR 18-SEP-1997; 97US-0059263P.
XX PR 18-SEP-1997; 97US-0059266P.
XX PR 17-OCT-1997; 97US-0062250P.
XX PR 21-OCT-1997; 97US-0063486P.
XX PR 24-OCT-1997; 97US-0063120P.

KW prostate tumour; rectal tumour; cervical tumour; liver tumour.

OS Homo sapiens.

XX US2003032127-A1.

PN 13-FEB-2003.

XX 26-JUN-2002; 2002US-00183012.

XX 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 17-OCT-1997; 97US-0082250P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063112P.

PR 28-OCT-1997; 97US-0063540P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-0063734P.

PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.

PR 13-NOV-1997; 97US-0085311P.

PR 21-NOV-1997; 97US-0086120P.

PR 24-NOV-1997; 97US-0066466P.

PR 24-NOV-1997; 97US-0066772P.

PR 11-DEC-1997; 97US-0069335P.

PR 12-DEC-1997; 97US-0069425P.

PR 17-DEC-1997; 97US-0069870P.

PR 18-DEC-1997; 97US-0068017P.

PR 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077632P.

PR 11-MAR-1998; 98US-0077649P.

PR 20-MAR-1998; 98US-0078886P.

PR 20-MAR-1998; 98US-0078939P.

PR 27-MAR-1998; 98US-0079664P.

PR 27-MAR-1998; 98US-0079786P.

PR 31-MAR-1998; 98US-0080107P.

PR 31-MAR-1998; 98US-0080194P.

PR 01-APR-1998; 98US-0080327P.

PR 01-APR-1998; 98US-0080333P.

PR 08-APR-1998; 98US-0081049P.

PR 08-APR-1998; 98US-0081070P.

PR 09-APR-1998; 98US-0081195P.

PR 04-JUN-1998; 98US-0088028P.

PR 04-JUN-1998; 98US-0088029P.

PR 04-JUN-1998; 98US-0088033P.

PR 05-JUN-1998; 98US-0088326P.

PR 05-JUN-1998; 98US-0088167P.

PR 05-JUN-1998; 98US-0088202P.

PR 05-JUN-1998; 98US-0088212P.

PR 05-JUN-1998; 98US-0088217P.

PR 09-JUN-1998; 98US-0088655P.

PR 10-JUN-1998; 98US-0088722P.

PR 10-JUN-1998; 98US-0088738P.

PR 10-JUN-1998; 98US-0088740P.

PR 10-JUN-1998; 98US-0088811P.

PR 10-JUN-1998; 98US-0088824P.

PR 10-JUN-1998; 98US-0088825P.

PR 10-JUN-1998; 98US-0088826P.

PR 11-JUN-1998; 98US-0088861P.

PR 11-JUN-1998; 98US-0088863P.

PR 11-JUN-1998; 98US-0088876P.

PR 12-JUN-1998; 98US-0089090P.

PR 12-JUN-1998; 98US-0089105P.

PR 16-JUN-1998; 98US-0089512P.

PR 16-JUN-1998; 98US-0089514P.

PR 17-JUN-1998; 98US-0089538P.

PR 17-JUN-1998; 98US-0089598P.

PR 17-JUN-1998; 98US-0089653P.

PR 18-JUN-1998; 98US-0089908P.

PR 19-JUN-1998; 98US-0089952P.

PR 22-JUN-1998; 98US-0090246P.

PR 22-JUN-1998; 98US-0090252P.

PR 22-JUN-1998; 98US-0090254P.

PR 24-JUN-1998; 98US-0090429P.

PR 24-JUN-1998; 98US-0090435P.

PR 24-JUN-1998; 98US-0090444P.

PR 24-JUN-1998; 98US-0090461P.

PR 24-JUN-1998; 98US-0090535P.

PR 24-JUN-1998; 98US-0090540P.

PR 25-JUN-1998; 98US-0090676P.

PR 25-JUN-1998; 98US-0090678P.

PR 25-JUN-1998; 98US-0090688P.

PR 25-JUN-1998; 98US-0090690P.

PR 25-JUN-1998; 98US-0090694P.

PR 25-JUN-1998; 98US-0090695P.

PR 25-JUN-1998; 98US-0090696P.

PR 26-JUN-1998; 98US-00105413.

PR 26-JUN-1998; 98US-0090862P.

PR 26-JUN-1998; 98US-0090863P.

PR 26-JUN-1998; 98US-0091010P.

PR 01-JUL-1998; 98US-0091359P.

PR 02-JUL-1998; 98US-0091544P.

PR 02-JUL-1998; 98US-0091478P.

PR 02-JUL-1998; 98US-0091486P.

PR 02-JUL-1998; 98US-0091626P.

PR 02-JUL-1998; 98US-0091628P.

PR 02-JUL-1998; 98US-0091632P.

PR 04-AUG-1998; 98US-0094006P.

PR 10-AUG-1998; 98US-0095282P.

PR 10-AUG-1998; 98US-0095998P.

PR 10-AUG-1998; 98US-0096012P.

PR 17-AUG-1998; 98US-0096757P.

PR 17-AUG-1998; 98US-0096766P.

PR 17-AUG-1998; 98US-0096867P.

PR 17-AUG-1998; 98US-0096891P.

PR 17-AUG-1998; 98US-0096897P.

PR 18-AUG-1998; 98US-0096949P.

PR 18-AUG-1998; 98US-0096959P.

PR 18-AUG-1998; 98US-0097022P.

PR 26-AUG-1998; 98US-0097952P.

PR 26-AUG-1998; 98US-0097954P.

PR 26-AUG-1998; 98US-0097955P.

PR 26-AUG-1998; 98US-0097971P.

PR 26-AUG-1998; 98US-0097974P.

PR 26-AUG-1998; 98US-0098014P.

PR	01-SEP-1998;	98US-0098716P.	ABU84388	
PR	01-SEP-1998;	98US-0098723P.	ID	ABU84388 standard; protein; 363 AA.
PR	02-SEP-1998;	98US-0098803P.	XX	
PR	02-SEP-1998;	98US-0098821P.	AC	ABU84388;
PR	02-SEP-1998;	98US-0098843P.	XX	
PR	09-SEP-1998;	98US-0099602P.	DT	02-AUG-2003 (first entry)
PR	10-SEP-1998;	98US-0099741P.	XX	Human secreted/transmembrane protein (PRO) #126.
PR	10-SEP-1998;	98US-0099763P.	DE	
PR	10-SEP-1998;	98US-0099812P.	XX	Human; secreted and transmembrane protein; PRO; TNF-alpha;
PR	15-SEP-1998;	98US-0100388P.	KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
PR	16-SEP-1998;	98US-0100662P.	KW	tissue typing.
PR	16-SEP-1998;	98US-0100664P.	XX	
PR	16-SEP-1998;	98US-0101751P.	OS	Homo sapiens.
PR	16-SEP-1998;	98US-0101933P.	XX	
PR	17-SEP-1998;	98US-0100683P.	XX	US2003032112-A1.
PR	17-SEP-1998;	98US-0100684P.	PD	13-FEB-2003.
PR	17-SEP-1998;	98US-0100919P.	XX	
PR	17-SEP-1998;	98US-0100930P.	XX	21-JUN-2002; 2002US-00176756.
PR	18-SEP-1998;	98US-0100849P.	XX	
PR	18-SEP-1998;	98US-0101014P.	PR	18-SEP-1997; 97US-0059263P.
PR	18-SEP-1998;	98US-0101068P.	PR	18-SEP-1997; 97US-0059266P.
PR	23-SEP-1998;	98US-0101471P.	PR	17-OCT-1997; 97US-0062250P.
PR	23-SEP-1998;	98US-0101472P.	PR	21-OCT-1997; 97US-0063486P.
PR	23-SEP-1998;	98US-0101475P.	PR	24-OCT-1997; 97US-0063120P.
PR	23-SEP-1998;	98US-0101477P.	PR	24-OCT-1997; 97US-0063121P.
PR	24-SEP-1998;	98US-0101738P.	PR	28-OCT-1997; 97US-0063540P.
PR	24-SEP-1998;	98US-0101739P.	PR	28-OCT-1997; 97US-0063541P.
PR	24-SEP-1998;	98US-0101743P.	PR	28-OCT-1997; 97US-0063544P.
PR	24-SEP-1998;	98US-0101942P.	PR	28-OCT-1997; 97US-0063564P.
PR	25-SEP-1998;	98US-0101786P.	PR	29-OCT-1997; 97US-0063734P.
PR	29-SEP-1998;	98US-0102207P.	PR	31-OCT-1997; 97US-0063870P.
PR	29-SEP-1998;	98US-0102240P.	PR	31-OCT-1997; 97US-0064103P.
PR	29-SEP-1998;	98US-0102330P.	PR	31-OCT-1997; 97US-0065311P.
PR	29-SEP-1998;	98US-0102331P.	PR	13-NOV-1997; 97US-0066120P.
PR	29-SEP-1998;	98US-0102487P.	PR	21-NOV-1997; 97US-0066466P.
PR	30-SEP-1998;	98US-0102570P.	PR	24-NOV-1997; 97US-0066772P.
PR	30-SEP-1998;	98US-0102571P.	PR	24-NOV-1997; 97US-0069335P.
PR	01-OCT-1998;	98US-0102684P.	PR	12-DEC-1997; 97US-0069425P.
PR	01-OCT-1998;	98US-0102687P.	PR	17-DEC-1997; 97US-0069870P.
PR	02-OCT-1998;	98US-0102965P.	PR	18-DEC-1997; 97US-0068017P.
PR	06-OCT-1998;	98US-0103258P.	PR	10-MAR-1998; 98US-0077450P.
PR			PR	11-MAR-1998; 98US-0077632P.
PR			PR	11-MAR-1998; 98US-0077649P.
PR			PR	20-MAR-1998; 98US-0078886P.
PR			PR	20-MAR-1998; 98US-0078939P.
PR			PR	27-MAR-1998; 98US-0079664P.
PR			PR	27-MAR-1998; 98US-0079786P.
PR			PR	31-MAR-1998; 98US-0080107P.
PR			PR	31-MAR-1998; 98US-0080194P.
PR			PR	01-APR-1998; 98US-0080327P.
PR			PR	01-APR-1998; 98US-0080333P.
PR			PR	08-APR-1998; 98US-0081049P.
PR			PR	08-APR-1998; 98US-0081070P.
PR			PR	09-APR-1998; 98US-0081195P.
PR			PR	09-APR-1998; 98US-0081838P.
PR			PR	15-APR-1998; 98US-0082568P.
PR			PR	21-APR-1998; 98US-0082569P.
PR			PR	21-APR-1998; 98US-0082704P.
PR			PR	22-APR-1998; 98US-0082797P.
PR			PR	28-APR-1998; 98US-0083322P.
PR			PR	29-APR-1998; 98US-0083495P.
PR			PR	29-APR-1998; 98US-0083496P.
PR			PR	29-APR-1998; 98US-0083499P.
PR			PR	29-APR-1998; 98US-0083559P.
PR			PR	05-MAY-1998; 98US-0084366P.
PR			PR	06-MAY-1998; 98US-0084414P.
PR			PR	07-MAY-1998; 98US-0084639P.
PR			PR	07-MAY-1998; 98US-0084640P.
PR			PR	07-MAY-1998; 98US-0084643P.
PR			PR	15-MAY-1998; 98US-0085579P.
PR			PR	15-MAY-1998; 98US-0085580P.

Query Match 37.9%; Score 1536; DB 6; Length 363;

Db	189	ASAVENPGSGADVTGLNVQFCALEFGSEPSLSEFGSAPSENENQIPISLYSKSLSEPLNT	248	15-APR-1998; PR
Qy	245	SLSMTSVAVQNSTYTTTSVITTSLSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYOSPVSSES	304	15-APR-1998; PR
Db	249	SLSMTSVAVQNSTYTTTSVITTSLSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYOSPVSSES	308	21-APR-1998; PR
Qy	305	APGTIMNHGGGRSQOTLDT	324	21-APR-1998; PR
Db	309	APGTIMNHGGGRSQOTLDS	328	22-APR-1998; PR
RESULT 11				28-APR-1998; PR
ABR66262				29-APR-1998; PR
ID	ABR66262	standard; protein; 363 AA.		29-APR-1998; PR
XX	AC			29-APR-1998; PR
XX	AX			05-MAY-1998; PR
XX	DT			06-MAY-1998; PR
XX	DE			07-MAY-1998; PR
XX	XX			07-MAY-1998; PR
XX	XX			07-MAY-1998; PR
KW	KW	Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnuary; gene therapy.		07-MAY-1998; PR
XX	XX	Homo sapiens.		07-MAY-1998; PR
XX	XX	US2003027278-A1.		07-MAY-1998; PR
XX	XX	06-FEB-2003.		07-MAY-1998; PR
XX	XX	21-JUN-2002; 2002US-00176987.		07-MAY-1998; PR
XX	XX	18-SEP-1997; 97US-0059263P.		07-MAY-1998; PR
PR	PR	18-SEP-1997; 97US-0059266P.		07-MAY-1998; PR
PR	PR	17-OCT-1997; 97US-0062250P.		07-MAY-1998; PR
PR	PR	21-OCT-1997; 97US-0063486P.		07-MAY-1998; PR
PR	PR	24-OCT-1997; 97US-0063120P.		07-MAY-1998; PR
PR	PR	24-OCT-1997; 97US-0063121P.		07-MAY-1998; PR
PR	PR	28-OCT-1997; 97US-0063540P.		07-MAY-1998; PR
PR	PR	28-OCT-1997; 97US-0063541P.		07-MAY-1998; PR
PR	PR	28-OCT-1997; 97US-0063544P.		07-MAY-1998; PR
PR	PR	28-OCT-1997; 97US-0063564P.		07-MAY-1998; PR
PR	PR	31-OCT-1997; 97US-0063734P.		07-MAY-1998; PR
PR	PR	31-OCT-1997; 97US-0063870P.		07-MAY-1998; PR
PR	PR	31-OCT-1997; 97US-0064103P.		07-MAY-1998; PR
PR	PR	13-NOV-1997; 97US-0085311P.		07-MAY-1998; PR
PR	PR	21-NOV-1997; 97US-00866120P.		07-MAY-1998; PR
PR	PR	24-NOV-1997; 97US-0066466P.		07-MAY-1998; PR
PR	PR	24-NOV-1997; 97US-0066772P.		07-MAY-1998; PR
PR	PR	11-DEC-1997; 97US-0069335P.		07-MAY-1998; PR
PR	PR	12-DEC-1997; 97US-0069425P.		07-MAY-1998; PR
PR	PR	17-DEC-1997; 97US-0069870P.		07-MAY-1998; PR
PR	PR	18-DEC-1997; 97US-0068017P.		07-MAY-1998; PR
PR	PR	10-MAR-1998; 98US-0077450P.		07-MAY-1998; PR
PR	PR	11-MAR-1998; 98US-0077632P.		07-MAY-1998; PR
PR	PR	11-MAR-1998; 98US-0077649P.		07-MAY-1998; PR
PR	PR	20-MAR-1998; 98US-0078886P.		07-MAY-1998; PR
PR	PR	20-MAR-1998; 98US-0078939P.		07-MAY-1998; PR
PR	PR	27-MAR-1998; 98US-0079664P.		07-MAY-1998; PR
PR	PR	27-MAR-1998; 98US-0079786P.		07-MAY-1998; PR
PR	PR	31-MAR-1998; 98US-0080107P.		07-MAY-1998; PR
PR	PR	31-MAR-1998; 98US-0080194P.		07-MAY-1998; PR
PR	PR	01-APR-1998; 98US-0080327P.		07-MAY-1998; PR
PR	PR	01-APR-1998; 98US-0080333P.		07-MAY-1998; PR
PR	PR	08-APR-1998; 98US-0081049P.		07-MAY-1998; PR
PR	PR	08-APR-1998; 98US-0081070P.		07-MAY-1998; PR
PR	PR	08-APR-1998; 98US-0081195P.		07-MAY-1998; PR

PR	26-JUN-1998;	98US-0090862P.
PR	26-JUN-1998;	98US-0090863P.
PR	26-JUN-1998;	98US-0091010P.
PR	01-JUL-1998;	98US-0091359P.
PR	01-JUL-1998;	98US-0091544P.
PR	02-JUL-1998;	98US-0091478P.
PR	02-JUL-1998;	98US-0091486P.
PR	02-JUL-1998;	98US-0091626P.
PR	02-JUL-1998;	98US-0091628P.
PR	02-JUL-1998;	98US-0091632P.
PR	04-AUG-1998;	98US-0094006P.
PR	04-AUG-1998;	98US-0095282P.
PR	10-AUG-1998;	98US-0095998P.
PR	10-AUG-1998;	98US-0096012P.
PR	17-AUG-1998;	98US-0096757P.
PR	17-AUG-1998;	98US-0096766P.
PR	17-AUG-1998;	98US-0096867P.
PR	17-AUG-1998;	98US-0096881P.
PR	17-AUG-1998;	98US-0096897P.
PR	18-AUG-1998;	98US-0096949P.
PR	18-AUG-1998;	98US-0096959P.
PR	18-AUG-1998;	98US-0097022P.
PR	26-AUG-1998;	98US-0097952P.
PR	26-AUG-1998;	98US-0097954P.
PR	26-AUG-1998;	98US-0097955P.
PR	26-AUG-1998;	98US-0097971P.
PR	26-AUG-1998;	98US-0097974P.
PR	26-AUG-1998;	98US-0098014P.
PR	01-SEP-1998;	98US-0098716P.
PR	01-SEP-1998;	98US-0098723P.
PR	02-SEP-1998;	98US-0098803P.
PR	02-SEP-1998;	98US-0098821P.
PR	02-SEP-1998;	98US-0098843P.
PR	09-SEP-1998;	98US-0099602P.
PR	10-SEP-1998;	98US-0099741P.
PR	10-SEP-1998;	98US-0099754P.
PR	10-SEP-1998;	98US-0099763P.
PR	10-SEP-1998;	98US-0099812P.
PR	15-SEP-1998;	98US-0100388P.
PR	16-SEP-1998;	98US-0100662P.
PR	16-SEP-1998;	98US-0100664P.
PR	16-SEP-1998;	98US-0101751P.
PR	16-SEP-1998;	98US-0101751P.
PR	16-SEP-1998;	98US-0101933P.
PR	17-SEP-1998;	98US-0100683P.
PR	17-SEP-1998;	98US-0100684P.
PR	17-SEP-1998;	98US-0100919P.
PR	17-SEP-1998;	98US-0100930P.
PR	17-SEP-1998;	98US-0100849P.
PR	18-SEP-1998;	98US-0101014P.
PR	18-SEP-1998;	98US-0101068P.
PR	23-SEP-1998;	98US-0101471P.
PR	23-SEP-1998;	98US-0101472P.
PR	23-SEP-1998;	98US-0101475P.
PR	23-SEP-1998;	98US-0101477P.
PR	24-SEP-1998;	98US-0101738P.
PR	24-SEP-1998;	98US-0101739P.
PR	24-SEP-1998;	98US-0101743P.
PR	24-SEP-1998;	98US-0101922P.
PR	25-SEP-1998;	98US-0101786P.
PR	29-SEP-1998;	98US-0102207P.
PR	29-SEP-1998;	98US-0102240P.
PR	29-SEP-1998;	98US-0102330P.
PR	29-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102487P.
PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.

Query Match

Best Local Similarity

Matches 308; Conservative

37.9%; Score 1536; DB 6; Length 363;

96.2%; Pred. No. 1.3e-84;

3; Mismatches 7; Indels 2; Gaps 1;

Qy	7	SSTAVNSCS--PQSLSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQON	64
Db	9	NSVLLRICSFPLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQON	68
Qy	65	STSHPTTTTSDWLKPPPTSSQSVLSHLDFKSPSPVLSQLSQOQHQSQAQVTPPPGLE	124
Db	69	STSHPTTTTSDWLKPPPTSSQSVLSHLDFKSPSPVLSQLSQOQHQSQAQVTPPPGLE	128
Qy	125	SPPSOAKLRESTPGDSPSTVNVKLLQLPSTTTIENISVSVHQPQPKHILAKRRIIPASKIP	184
Db	129	SPPSOAKLRESTPGDSPSTVNVKLLQLPSTTTIENISVSVHQPQPKHILAKRRIIPASKIP	188
Qy	185	ASAVEMPGSADVTGLNVQFGALEFSGSEPSLSEFSGSAPSSSENSQIPISLYSKSLSEPLNT	244
Db	189	ASAVEMPGSADVTGLNVQFGALEFSGSEPSLSEFSGSAPSSSENSQIPISLYSKSLSEPLNT	248
Qy	245	SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES	304
Db	249	SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES	308
Qy	305	APGTTMNGHGGRSQQTLDLT	324
Db	309	APGTTMNGHGGRSQQTILDS	328
RESULT 12			
ABR65652			
ID	ABR65652 standard; protein; 363 AA.		
AC	ABR65652;		
XX	05-AUG-2003 (first entry)		
DT	Human secreted polypeptide PRO1197, SEQ ID NO.252.		
DE	Human; PRO; secreted protein; transmembrane protein;		
XX	extracellular domain; tumour necrosis factor-alpha; TNF-alpha;		
KW	chondrocyte; proliferation; differentiation; cartilage disorder;		
KW	bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;		
KW	adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;		
KW	liver; drug screening; transgenic animal; genetic analysis;		
KW	antiarthritic; vulnery; gene therapy.		
XX	Homo sapiens.		
OS	US2003036159-A1.		
XX	20-FEB-2003.		
XX	02-JUL-2002; 2002US-00188773.		
XX	18-SEP-1997; 97US-0059263P.		
PR	18-SEP-1997; 97US-0059266P.		
PR	17-OCT-1997; 97US-0062250P.		
PR	21-OCT-1997; 97US-0063486P.		
PR	24-OCT-1997; 97US-0063120P.		
PR	24-OCT-1997; 97US-0063121P.		
PR	28-OCT-1997; 97US-0063540P.		
PR	28-OCT-1997; 97US-0063541P.		
PR	28-OCT-1997; 97US-0063544P.		
PR	28-OCT-1997; 97US-0063564P.		
PR	29-OCT-1997; 97US-0063734P.		
PR	31-OCT-1997; 97US-0063870P.		
PR	31-OCT-1997; 97US-0064103P.		
PR	13-NOV-1997; 97US-0065311P.		
PR	21-NOV-1997; 97US-0066120P.		
PR	24-NOV-1997; 97US-0066466P.		
PR	24-NOV-1997; 97US-0066772P.		
PR	11-DEC-1997; 97US-0069335P.		
PR	12-DEC-1997; 97US-0069425P.		
PR	17-DEC-1997; 97US-0069870P.		
PR	18-DEC-1997; 97US-0068017P.		
PR	10-MAR-1998; 98US-0077450P.		

Query Match 37.9%; Score 1536; DB 6; Length 363;
Best Local Similarity 96.2%; Pred. No. 1.3e-84;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

us-10-509-307-1.rag

Wed Feb 2 13:56:23 2005

PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078931P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 28-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088730P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089511P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.

PR	17-JUN-1998;	98US-0089538P.
PR	17-JUN-1998;	98US-0089598P.
PR	17-JUN-1998;	98US-0101475P.
PR	17-JUN-1998;	98US-0101477P.
PR	18-JUN-1998;	98US-0089653P.
PR	18-JUN-1998;	98US-0089908P.
PR	19-JUN-1998;	98US-0089952P.
PR	19-JUN-1998;	98US-0090246P.
PR	22-JUN-1998;	98US-0090252P.
PR	22-JUN-1998;	98US-0090254P.
PR	22-JUN-1998;	98US-0090429P.
PR	24-JUN-1998;	98US-0090435P.
PR	24-JUN-1998;	98US-0090461P.
PR	24-JUN-1998;	98US-0090535P.
PR	24-JUN-1998;	98US-0090540P.
PR	24-JUN-1998;	98US-0090429P.
PR	24-JUN-1998;	98US-0090444P.
PR	24-JUN-1998;	98US-0090461P.
PR	24-JUN-1998;	98US-0090535P.
PR	24-JUN-1998;	98US-0090540P.
PR	25-JUN-1998;	98US-0090676P.
PR	25-JUN-1998;	98US-0090688P.
PR	25-JUN-1998;	98US-0090690P.
PR	25-JUN-1998;	98US-0090694P.
PR	25-JUN-1998;	98US-0090695P.
PR	25-JUN-1998;	98US-0090696P.
PR	26-JUN-1998;	98US-00105413.
PR	26-JUN-1998;	98US-0090862P.
PR	26-JUN-1998;	98US-0090863P.
PR	26-JUN-1998;	98US-0091010P.
PR	26-JUN-1998;	98US-0091359P.
PR	01-JUL-1998;	98US-0091478P.
PR	01-JUL-1998;	98US-0091486P.
PR	02-JUL-1998;	98US-0091626P.
PR	02-JUL-1998;	98US-0091628P.
PR	02-JUL-1998;	98US-0091632P.
PR	02-JUL-1998;	98US-0091633P.
PR	04-AUG-1998;	98US-0095282P.
PR	10-AUG-1998;	98US-0095998P.
PR	10-AUG-1998;	98US-0096012P.
PR	17-AUG-1998;	98US-0096757P.
PR	17-AUG-1998;	98US-0096766P.
PR	17-AUG-1998;	98US-0096867P.
PR	17-AUG-1998;	98US-0096891P.
PR	17-AUG-1998;	98US-0096897P.
PR	18-AUG-1998;	98US-0096949P.
PR	18-AUG-1998;	98US-0096959P.
PR	18-AUG-1998;	98US-0097032P.
PR	26-AUG-1998;	98US-0097952P.
PR	26-AUG-1998;	98US-0097954P.
PR	26-AUG-1998;	98US-0097955P.
PR	26-AUG-1998;	98US-0097971P.
PR	26-AUG-1998;	98US-0097974P.
PR	26-AUG-1998;	98US-0098014P.
PR	01-SEP-1998;	98US-0098716P.
PR	01-SEP-1998;	98US-0098723P.
PR	02-SEP-1998;	98US-0098803P.
PR	02-SEP-1998;	98US-0098821P.
PR	02-SEP-1998;	98US-0098843P.
PR	09-SEP-1998;	98US-0099602P.
PR	10-SEP-1998;	98US-0099741P.
PR	10-SEP-1998;	98US-0099754P.
PR	10-SEP-1998;	98US-0099763P.
PR	10-SEP-1998;	98US-0099812P.
PR	15-SEP-1998;	98US-0100389P.
PR	16-SEP-1998;	98US-0100662P.
PR	16-SEP-1998;	98US-0100664P.
PR	16-SEP-1998;	98US-0101751P.
PR	16-SEP-1998;	98WO-US019330.
PR	17-SEP-1998;	98US-0100683P.
PR	17-SEP-1998;	98US-0100684P.
PR	17-SEP-1998;	98US-0100919P.
PR	17-SEP-1998;	98US-0100930P.
PR	18-SEP-1998;	98US-0100849P.
PR	18-SEP-1998;	98US-0101014P.
PR	18-SEP-1998;	98US-0101068P.
PR	23-SEP-1998;	98US-0101471P.
PR	23-SEP-1998;	98US-0101472P.
PR	23-SEP-1998;	98US-0101475P.
PR	23-SEP-1998;	98US-0101477P.
PR	24-SEP-1998;	98US-0101738P.
PR	24-SEP-1998;	98US-0101739P.
PR	24-SEP-1998;	98US-0101743P.
PR	24-SEP-1998;	98US-0101922P.
PR	25-SEP-1998;	98US-0101786P.
PR	29-SEP-1998;	98US-0102207P.
PR	29-SEP-1998;	98US-0102240P.
PR	29-SEP-1998;	98US-0102330P.
PR	29-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102487P.
PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.
PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.
PR	06-OCT-1998;	98US-0103449P.
PR	07-OCT-1998;	98US-00168978.
Query Match 37.9%; Score 1536; DB 6; Length 363;		
Best Local Similarity 96.2%; Pred. No. 1.3e-84;		
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;		
QY	7 SSTAVNSCS--POSLSVLSGFGELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQON	64
Db	9 NSVLIRICSFIPLLKSSVLSGFGELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQON	68
QY	65 STSHPTTTTSDLPKPTQSQSVLSHLDFKSPVLSQLSQROHQSOAVTPPPGLE	124
Db	69 STSHPTTTTSDLPKPTQSQSVLSHLDFKSPVLSQLSQROHQSOAVTPPPGLE	128
QY	125 SFPQAKLRSTPGDSPSTVANKLLQLPSTTIENISVHQPKHIIKLAKRIPPASKIP	184
Db	129 SFPQAKLRSTPGDSPSTVANKLLQLPSTTIENISVHQPKHIIKLAKRIPPASKIP	188
QY	185 ASAVEMPGSADVTGLNVQFGALEFGSEPSLSBFGSAPSENSNQIPISLYSKSLSEPLNT	244
Db	189 ASAVEMPGSADVTGLNVQFGALEFGSEPSLSBFGSAPSENSNQIPISLYSKSLSEPLNT	248
QY	245 SLSMTSAVQNSTYTTTSVITSCSLTSSLSNSASPVMSSSYDOSSVHNRIPIQSPVSSSES	304
Db	249 SLSMTSAVQNSTYTTTSVITSCSLTSSLSNSASPVMSSSYDOSSVHNRIPIQSPVSSSES	308
QY	305 APTGTMNGHGGRSQOTLDT	324
Db	309 APTGTMNGHGGRSQOTLDS	328
RESULT 14		
ABU82831		
ID	ABU82831 standard; protein; 363 AA.	
XX		
AC	ABU82831;	
XX		
DT	27-JUN-2003 (first entry)	
XX		
DE	Human PRO polypeptide #126.	
XX		
KW	Human; PRO polypeptide; secreted and transmembrane protein; tumour;	
KW	chromosome mapping; gene mapping; cytostatic.	
OS	Homo sapiens.	
XX		
PN	US2003032113-A1.	
XX		
PD	13-FEB-2003.	
XX		
PF	20-JUN-2002; 2002US-00176911.	
XX		
PR	18-SEP-1997; 97US-0059263P.	

PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0064103P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069333P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078933P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081043P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 06-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.

PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.

PR	16-SEP-1998;	98US-0100662P.	XX	Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;
PR	16-SEP-1998;	98US-0100664P.	KW	chondrocyte differentiation; tumour necrosis factor-alpha release;
PR	16-SEP-1998;	98US-0101751P.	KW	affinity purification.
PR	16-SEP-1998;	98WO-US010330.	XX	
PR	17-SEP-1998;	98US-0100683P.	OS	Homo sapiens.
PR	17-SEP-1998;	98US-0100684P.	XX	
PR	17-SEP-1998;	98US-0100919P.	PN	US2003036147-A1.
PR	17-SEP-1998;	98US-0100849P.	XX	
PR	18-SEP-1998;	98US-0101014P.	PD	20-FEB-2003.
PR	18-SEP-1998;	98US-0101068P.	XX	
PR	18-SEP-1998;	98US-0101471P.	XX	02-JUL-2002; 2002US-00187741.
PR	23-SEP-1998;	98US-0101472P.	PR	18-SEP-1997; 97US-0059263P.
PR	23-SEP-1998;	98US-0101475P.	PR	18-SEP-1997; 97US-0059266P.
PR	23-SEP-1998;	98US-0101477P.	PR	17-OCT-1997; 97US-0062250P.
PR	24-SEP-1998;	98US-0101738P.	PR	21-OCT-1997; 97US-0063486P.
PR	24-SEP-1998;	98US-0101739P.	PR	24-OCT-1997; 97US-0063120P.
PR	24-SEP-1998;	98US-0101743P.	PR	24-OCT-1997; 97US-0063121P.
PR	24-SEP-1998;	98US-0101922P.	PR	28-OCT-1997; 97US-0063540P.
PR	25-SEP-1998;	98US-0101786P.	PR	28-OCT-1997; 97US-0063541P.
PR	29-SEP-1998;	98US-0102207P.	PR	28-OCT-1997; 97US-0063544P.
PR	29-SEP-1998;	98US-0102240P.	PR	28-OCT-1997; 97US-0063584P.
PR	29-SEP-1998;	98US-0102330P.	PR	28-OCT-1997; 97US-0063734P.
PR	29-SEP-1998;	98US-0102331P.	PR	29-OCT-1997; 97US-0063870P.
PR	30-SEP-1998;	98US-0102487P.	PR	31-OCT-1997; 97US-0064103P.
PR	30-SEP-1998;	98US-0102570P.	PR	13-NOV-1997; 97US-0065311P.
PR	30-SEP-1998;	98US-0102571P.	PR	21-NOV-1997; 97US-0066120P.
PR	01-OCT-1998;	98US-0102684P.	PR	24-NOV-1997; 97US-0066466P.
PR	01-OCT-1998;	98US-0102687P.	PR	24-NOV-1997; 97US-0066772P.
PR	02-OCT-1998;	98US-0102965P.	PR	11-MAR-1998; 98US-0077649P.
PR	06-OCT-1998;	98US-0103258P.	PR	11-MAR-1998; 98US-0078886P.
PR	06-OCT-1998;	98US-0103449P.	PR	20-MAR-1998; 98US-0078939P.
PR	07-OCT-1998;	98US-00168978.	PR	20-MAR-1998; 98US-0079664P.
PR	07-OCT-1998;	98US-0103395P.	PR	27-MAR-1998; 98US-0079786P.
PR	07-OCT-1998;		PR	27-MAR-1998; 98US-0080107P.
QY	7 SSTAIVSCS--PQSLSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQON 64		PR	31-MAR-1998; 98US-0080194P.
Db	9 NSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQON 68		PR	01-APR-1998; 98US-0080327P.
QY	65 STSHPTTTTNDLKPTQSSVLSHLDFKSPESVLSQLSORQCHQSOAVTVPPPGLE 124		PR	01-APR-1998; 98US-0080333P.
Db	69 STSHPTTTTNDLKPTQSSVLSHLDFKSPESVLSQLSORQCHQSOAVTVPPPGLE 128		PR	08-APR-1998; 98US-0081049P.
QY	125 SPFSQAKLRSTPGDSPSTVANKLLQLPSTTTIENISVSVHQPQPKHKLAKRIPPASKIP 184		PR	08-APR-1998; 98US-0081070P.
Db	129 SPFSQAKLRSTPGDSPSTVANKLLQLPSTTTIENISVSVHQPQPKHKLAKRIPPASKIP 188		PR	09-APR-1998; 98US-0081195P.
QY	185 ASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSPSSNSNQIPISLYSKSLSEPLNT 244		PR	15-APR-1998; 98US-0081838P.
Db	189 ASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSPSSNSNQIPISLYSKSLSEPLNT 248		PR	21-APR-1998; 98US-0082569P.
QY	245 SLSMTSAVONSRYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPYQSPVSSSES 304		PR	22-APR-1998; 98US-0082704P.
Db	249 SLSMTSAVONSRYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPYQSPVSSSES 308		PR	22-APR-1998; 98US-0082797P.
QY	305 APCTIMNGHGGRSQOTLDT 324		PR	28-APR-1998; 98US-0083322P.
Db	309 APCTIMNGHGGRSQOTLDS 328		PR	29-APR-1998; 98US-0083495P.
RESULT 15			PR	29-APR-1998; 98US-0083496P.
ID ABU89952			PR	29-APR-1998; 98US-0083499P.
XX ABU89952 standard; protein; 363 AA.			PR	29-APR-1998; 98US-0083559P.
AC ABU89952;			PR	05-MAY-1998; 98US-0084366P.
XX			PR	05-MAY-1998; 98US-0084414P.
XX			PR	07-MAY-1998; 98US-0084639P.
XX			PR	07-MAY-1998; 98US-0084640P.
XX			PR	07-MAY-1998; 98US-0084643P.
XX			PR	15-MAY-1998; 98US-0085579P.
XX			PR	15-MAY-1998; 98US-0085580P.
XX			PR	15-MAY-1998; 98US-0085582P.
XX			PR	15-MAY-1998; 98US-0085700P.
XX			PR	18-MAY-1998; 98US-0086023P.
XX			PR	22-MAY-1998; 98US-0086392P.
XX			PR	22-MAY-1998; 98US-0086486P.
XX			PR	28-MAY-1998; 98US-0087098P.
XX			PR	28-MAY-1998; 98US-0087208P.
DE	Novel human secreted and transmembrane protein PRO197.		PR	02-JUN-1998; 98US-0087609P.

Db 309 APGTIMNGHGGRSQOTLDS 328
|||||

Search completed: January 31, 2005, 17:43:30
Job time : 82 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 31, 2005, 17:39:37 ; Search time 24 Seconds
(without alignments)
2171.914 Million cell updates/sec

Title: US-10-509-307-1

Perfect score: 4055

Sequence: 1 MAPGTGSTAVNSCPSQLS.....LQPKSQASKPAYGNPWTN 786

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1248.5	30.8	983	4	US-09-538-092-1320
2	308.5	7.6	1140	4	US-09-538-092-647
3	289.5	7.1	1306	4	US-09-538-092-330
4	289	7.1	336	4	US-09-270-767-43343
5	287.5	7.1	2870	4	US-09-479-467A-15
6	287.5	7.1	3178	4	US-09-479-467A-4
7	286.5	7.1	2090	4	US-09-538-092-1081
8	282.5	7.0	2137	3	US-09-134-001C-4463
9	273.5	6.7	2972	3	US-09-579-181-2
10	273.5	6.7	3118	3	US-09-579-181-1
11	269	6.6	827	4	US-09-248-796A-17307
12	260.5	6.4	2004	4	US-09-854-856-58
13	260.5	6.4	2032	4	US-09-854-856-42
14	260.5	6.4	2064	4	US-09-854-856-26
15	260.5	6.4	2092	4	US-09-854-856-10
16	260.5	6.4	2141	4	US-09-854-856-56
17	260.5	6.4	2157	4	US-09-854-856-52
18	260.5	6.4	2169	4	US-09-854-856-40
19	260.5	6.4	2185	4	US-09-854-856-36
20	260.5	6.4	2201	4	US-09-854-856-24
21	260.5	6.4	2217	4	US-09-854-856-20
22	260.5	6.4	2229	4	US-09-854-856-8
23	260.5	6.4	2245	4	US-09-854-856-4
24	260.5	6.4	2294	4	US-09-854-856-50
25	260.5	6.4	2322	4	US-09-854-856-34
26	260.5	6.4	2354	4	US-09-854-856-18
27	260.5	6.4	2382	4	US-09-854-856-2

28	258.5	6.4	1911	4	US-09-854-856-64	Sequence 64, Appl
29	258.5	6.4	1939	4	US-09-854-856-48	Sequence 48, Appl
30	258.5	6.4	1971	4	US-09-854-856-32	Sequence 32, Appl
31	258.5	6.4	1999	4	US-09-854-856-16	Sequence 16, Appl
32	258.5	6.4	2048	4	US-09-854-856-62	Sequence 62, Appl
33	258.5	6.4	2076	4	US-09-854-856-46	Sequence 46, Appl
34	258.5	6.4	2108	4	US-09-854-856-30	Sequence 30, Appl
35	258.5	6.4	2136	4	US-09-854-856-14	Sequence 14, Appl
36	249.5	6.2	610	4	US-09-538-092-1378	Sequence 1378, Ap
37	249	6.1	1142	2	US-08-993-118-7	Sequence 7, Appl
38	249	6.1	1142	3	US-08-845-528C-7	Sequence 7, Appl
39	249	6.1	1142	4	US-09-066-281B-7	Sequence 7, Appl
40	249	6.1	1142	4	US-09-468-433C-7	Sequence 7, Appl
41	248.5	6.1	1093	3	US-08-545-860D-55	Sequence 55, Appl
42	248.5	6.1	1093	5	PCT-US94-04496-55	Sequence 55, Appl
43	246	6.1	1142	3	US-09-061-709-2	Sequence 2, Appl
44	246	6.1	1142	4	US-09-899-651-2	Sequence 2, Appl
45	246	6.1	1142	4	US-09-392-714-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1

US-09-538-092-1320
; Sequence 1320, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICATOR: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 1320
; LENGTH: 983
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q14157
US-09-538-092-1320

Query Match						30.8%; Score 1248.5; DB 4; Length 983;
Best Local Similarity						45.1%; Pred. No. 3.9e-76;
Matches						307; Conservative 98; Mismatches 188; Indels 87; Gaps 27;
Qy	3	PGTGSSTAVNSCPSQLS	VLGSGFGLAPPKMANITSSQILDQK-APSLGQFTTTPST	61		
Db	327	PASG----	NTFSHSHSVMSLKGFGDVGKAGSGTTGSGFLEQFKTAQALAA----	377		
Qy	62	QQNSTSHPTTTTNDLKPPTS	QSSVLSHLDFKQPEPSPVLSQSRQ-----	109		
Db	378	-QHSQSGSTTTSSWDM-	GSTTQPSLVQYDLDKN-PSDSAVHSPPTKQAPTPSSTMMEVF	434		
Qy	110	-QHSQNAV----	TVPPPGLESFPQAKLRSTGDSSTVNKLQLESTTIENSVSQHQ	164		
Db	435	LOEKSPAVATSTAAPP	PPSPPLPSKS---TSAPQMSFGSDNQSSP-----	479		
Qy	165	POPKHKLAKRRTPPASKI	PASAVEMPGSDVTLNVQFGLPEGSPSLSEFGSAP--SS	223		
Db	480	PAQOKLQKQKKASLTSKI	PALAVEMPGSADISGLNLFQFALQFGESEPVLSDYESTTTS	539		
Qy	224	ENSNQIPISLYKSLSEPLNT	SLSMTSVQNTYTTTSCVTSSTSSLSNASPVAMSSS	283		
Db	540	ASSSQAPSSLYTSTASBS	SSSTISSNQS--QESGYSQGPISQSTTTSQN-NAQGPL-----	591		

```
QY 284 YDOSSVHNRIPYQSPVSSSEAPGT-IMNGHGGGRSQOITLDTPKTGP-----PSALPSV 337
Db 592 YERQSTQTR-RYPSSISSSSQKDLTOAKNGFSSVQATQLQTTQSVGATGSAVKSDSPST 650
QY 338 SSLP-----STTSCALLPSTQHTG-----DLTSSPLSQLSSLSHQSLSAHAAL 385
Db 651 SSIPPLNETVSAASLLTTTQHSSSLGGLSHSEIPNTTTTQHSSSTLSTQOITLSSSTSS 710
QY 386 SSTSTHT--HAYVES-ASHQSGATFTSTAATSVSSASGCVLSLSSMNTANSICLGGTGA 442
Db 711 GRTSTLTLLTSVESEANLHSSSTFTSTSTVSAPPPV-VSVSSSLNCGSSLGLSLGN 769
QY 443 SASSSSRAAPLVTSKAPNLPQGVPPILLHNOYLVGPGGLLPAYP--IYGYDELOMLOS 500
Db 770 STVTASTRSVATTSKAPNLPQGVPPILLHNOYLVGPGGLLPAYP--IYGYDELOMLOS 500
QY 501 RLPVDYVIGIPFAAPTA-LASDRSLANNYPGVDVTKFGRGDSASAPATTPAQPOQSQQ 559
Db 829 RFLDYYSIPFPTPTPLTCRGLSLANPYSGDLTKFGRGDASSAPATTPAQPOQNQIQ 888
QY 560 THHTAQOPFVNPAIPGYSYTGILPYIT---CMPSAFQYGTMP-VPPASAKQHGVLNLS-- 613
Db 889 THHTQOTFLNPAIPGYSYTSIPYITGVGPLESTFYGPAPFPVAPTSSKQHGVLNLSV 948
QY 614 TPTPPFQOASGYGOGYSTG 633
Db 949 ASATPPQOPSGYSGHGINTG 968

RESULT 2
US-09-538-092-647
; Sequence 647, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538, 092
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-04-01
; PRIOR FILING DATE: 1999-04-01
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormer Version 0.9
; SEQ ID NO 647
; LENGTH: 1140
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YMR317W
US-09-538-092-647

Query Match
Best Local Similarity 7.6%; Score 308.5; DB 4; Length 1140;
Matches 210; Conservative 131; Mismatches 352; Indels 221; Gaps 36;

QY 4 GTGS--STANVSCPSQLSVLGSFGELAPPKWANIT-----SSOILDLKAPSLGQFT 56
Db 210 GTTSDASKEVFSSTSDSVLLSS-----TSSPASSTISETLPFSSTILSITSPVSEAP 265
QY 57 TTPSTQNSTSHPTTTTSDWKLPSTQSSVLHDLFKSQPEPVLSQLSQRQHQSOAV 116
Db 266 SATSSSVSSSEASSTSSVSSEAPLATSVVSS---EAPSTSSVVSSEAPSTSSSVSS 322
QY 117 TTPPPGLSPPSQAKUREST-----PGDSPVTNKLQLPSTTINIS-----V 160
Db 323 EISSTTSSSVSSSEAPLATSVVSSSEAPSTSSSVSS---EISSTTSSSVSSSEAPLATSVV 380

QY 161 SVHQPOPKHIKLAKRRIPPASKIPASAVEMPGSADVTGLNVQFALFEGFSEPSLSBFGSA 220
Db 381 SEAPSTSSSVSSSE--APSTSSSVSSSEAPSS---TSSSVSSSEISSTKSSVMSSEVSSA 435
QY 221 PSESNQIP---ISLYSKSLSEPLNTSMTSAVONSTYTTTSTVITSCSLTSSLSNASP 277
Db 436 TSSLVSSSEAPSAISSLASSRLFSKNTSVT-----STLVATEASSVITSSLRPSSSE 485
QY 278 VAMSSSYDOSSVHNRIPYQSPVSSSEAPGTIMNGHGGGRSQOITLDTPKTGPSPALPSV 337
Db 486 TLASNIIESSLT--GYNSTVITTTTSAASSTL-GSKVSSNSNRMAITSKTSSTSSLSKS 542
QY 338 SSIPSTTCTALLPSTQHTGTLSSPLSQLSSSL--SSHQSLSLSAHAALSSSTSHTHASV 396
Db 543 SVIFGNSVITVTPSASI---SLTASPLPSVMSDITSSSEASSISNLASSAPSDNNSTI 599
QY 397 EASG-----SHQSATFTSTAATSVSSASGVSLS--SNMTANSICLGG 439
Db 600 AGASLIVTKNSVSSIVSSITSETTINESLATSTSLSNKATARSILSTSNATSAN 659
QY 440 TPASASSSSRAAPLVTSKAPNLPQGVPPILLHNOYLVGPGGLLPAYPIYGYDELO--- 496
Db 660 VPTGTFSSMSHTSVITPGFTSSASLAINSTVSSSLAG-----YGFSTPESP 709
QY 497 ----MLQSLPVDYVIGIPPAAP-----TALASDRSLANNPY-PGVDVTKF 536
Db 710 TTSTLVTSEAPSTVSMTTTSAFINNSTSARPSPTASTFITESTSISVPLASGDT-- 767
QY 537 GRGDSASAPATTPAQPOQSQQ---THHTAQOPFVNPAIP-PGYSYTGILPYITGMPAS 592
Db 768 ---SSLAHNLATFSAPSTSSAQLVSKSTSSILVTPRIDRSGNSSTASRIATSLPN-- 822
QY 593 QYGPMTFVPP-----ASAKQ-----HGVNLSTPTPPF----- 619
Db 823 ---KTFVSSLSSTSAHARNIFNSTVLATAKQIETLTSTVNCNPPFNITKTIVSRE 879
QY 620 -----QOASGYGOGYSTGVDLITQ-----GTAAGDYSGGVAGSSQ 656
Db 880 TTAIGTVTSCSGCTKRXSTLITITDIDASTVTCPEKEVTSTSGDEAE--HTTSYK 937
QY 657 APN--KSAGSGPKGVSVSSSTTGLPDMTGVSVNKTQTQFDKGFHAGTTP-----PFSLP 709
Db 938 ISNFTSTPSESFKDMKTQETKAKPGSETVRSSSSFVEK-----TSPTTKASPTSP 991
QY 710 SVLGTG--PLASGAAPGYAPFPFLHILPAHQPHSQLLHHLPODAQSGSORSQSSSL 767
Db 992 SESKAAGNTSVATNASPTSP-----SESQGTGSTVEGA- 1026
QY 768 QPKSQASKPAYGNS 781
Db 1027 --KSKSTKNSEGV 1038

RESULT 3
US-09-538-092-330
; Sequence 330, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538, 092
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-04-01
; PRIOR FILING DATE: 1999-04-01
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormer Version 0.9
; SEQ ID NO 330
; LENGTH: 1306
; TYPE: PRT
```

```
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YGR014W
US-09-538-092-330

Query Match          7.1%; Score 289.5; DB 4; Length 1306;
Best Local Similarity 24.0%; Pred. No. 5e-11;
Matches 211; Conservative 110; Mismatches 365; Indels 193; Gaps 39;

Qy 2 APTGSSAVNSCPQLSSVLGSGFELAPPKANIT---SSQLDQ-----LKAPSL 52
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 180 APLTSDTPLISTMSADNFWSS-----APISASLTITDSSESFDTSTAGAIPOVSS 234
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 53 GQFTTT-----PSTQONSTGHPTTT-TSWDLKP-PTSQSS-----VLSHLDKFSQ 95
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 235 ADFSSSSRLVQSSADFSSPSTTTDLSAAPLOTSESSFTTASAAFPVSSTDVDS 294
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 96 PEPSPVLSQLQRQHQSQAVTPPPGLESPSQAKLRESTPGSPSTVKNKLQLP--ST 153
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 295 -SASPVS-MGAAGQIASSSTNDPTMGETFSLTS--TEVDGSDVSSSTVSALLSAPFLQT 350
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 154 TIENISVSHQPPQPHIKLAKRIPPASKIPA-SAVEMPGSADVTGLNVQFAL-----E 207
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 351 STSN-SF8IVGPS-----VSFVPSQSSSDVASSSTANVSSSFSDIPPQTST 396
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 208 FGSEPSLSEFGSAPSENNOIPISYKSLSEPLNTSLMSTSAVQNSTYTTTSVITCSL 267
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 397 SGSVVVAQASALAFQSTEV----YCASASTMSSLTSTS-LQSTLDSLSLASSA 451
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 268 TSSSL-----NSAPVAMSSSYDOSSVHNRIPYQSPVSS-----SESAPGTIMN 311
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 452 SSSDLTDYGVSTASIPLLSASEQAQSTSSFSVSPSVSFVPSQSSSDVASTSAPSVSS 511
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 312 G-----HGGRRSQTLTPKTGPPSPALPVSSLPSTTCTALLPSTQHTGDLTSSPL 365
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 512 SFSYTSLOAGSSMTNPSSSTTVYSSSTTGSSEESAASATASATLGSSTYTMAGNLQSQPP 571
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 366 SOLSSLSHQSLSAHAALSSSTSHT-----HASVE-----SASSHOSSTAFS 409
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 572 S-----TSSLSSEQATSTAVLASSSVSTSTPTTAGGASTEASSLSSTASTSQSVYSQS 629
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 410 TAATSVSSSASGV---SLSSMNTANSLCIGGTPASASSSSRAAPLVTSGKAPNLPQ 466
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 630 TTALQTSFASSTTEGSETSQGFSTSVLVQMPSSISSEFSPSQTTQMNSSASS--- 686
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 467 GVPPLLHNOYLVGCGLLP-----AYPIYGYDELQMLQRLPVDYIGIPFAPAPTALAS 519
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 687 -----SQYTSITSGILSQVSDTSVSXTTSSSSVSQV--SDTFVSY-----TTSSS 729
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 520 RDRSLANNPYPGDVTKFGRGDSAPAPATTTPAQPOQSQTHHTAQQPFVNPALPPGVSY 579
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 730 SVSQVSDTP-----VSYTTSSSSVSQVSDTPVSTTTSSSSVSQVSDTP----- 772
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 580 TGLPYTGMPGAFQVPTFMFPASAKQGVNLS-TPTPPQASGQGHGYSTGYDDLT 638
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 773 --VSYTTSSSSVSQVSDTS-VPTSSRSSVSQVSDTPVPTSSRSSVSQ--TSSSLQPTT 827
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 639 QGTAAGDYKGYAGSQAPNKSAGSGPGKGVSVSSSTTGLPDMTGVYNNKTQFDKQGF 698
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 828 TSSORFTTSTHGALSSSSVSQQA-----SEITSSINATASEYHSIQT----- 870
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 699 HAGTPTTTPSLPVLGSGTGLASGAPGAPPFPLHILPAHQPHSQLL-----HHHLQDA 754
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 871 TAAATQ-----STLTSFTDANSSAS---APLEVATSTPTPSKASSLLLTPTSTSSLSQVA 922
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 755 QSGSGQRS-----OPSSLOPKSQASKPAYGNSPYW 784
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 923 TTNVQISLTSTTVLEPSTTNSSSTFSLTSSDNNW 961
```

RESULT 4

```
US-09-270-767-43343
; Sequence 43343, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43343
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43343

Query Match          7.1%; Score 289; DB 4; Length 336;
Best Local Similarity 31.5%; Pred. No. 8.3e-12;
Matches 98; Conservative 44; Mismatches 103; Indels 66; Gaps 19;

Qy 491 GYDELMQLQRLPYDYGIFPAAPTALASRRDRSLANNPYPGDVT-----KFGRGD-SA 542
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 543 SPAPATTPAQPOQSQSTHTHTAQQPFVNPALPCYSYTGTPYTGMPSAFOYG-PTMFVP 601
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 83 SPGVNVSSTWSQQGSSA-----PMLN--VPYAYFYGG---NMPGSGFYSTPAIYLQ 130
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 602 -PASAKQGVNLSPTTFFQOASGQGHGYSTGYDLDLTQGTAAAGDYKGYAGSSQAPNK 660
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 131 IPAANTASGQFPKPS-----YSAGYG---STSDTILSQTQ--DYSKGGYSSSVNQSK 180
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 661 SAGSGPKGVSVSSSTTGLPDMTGSVY-----NKTQTFDKQGFHAGTTPPPFSLPSVLG 713
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 181 T-----QTVSNOSQAGTSGDLTSSMTYKGVHVALNKVSEKQSFHSGTTPPPFNNPN--- 231
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 714 STGPLASGAAPGVAPPFPLHILPAHQPHSOLLHHLLPQDAQSGSGORSOPSSLOPKSOA 773
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 232 -----TQTAGGTSQAQPYGMPLPMPAAGHHNMHIQPIHQDSNS-AGORQOSTS-QSKS-A 282
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 774 SKPAYGNSPYW 784
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 283 GKQGYSPS-YW 292
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 5
US-09-479-467A-15
; Sequence 15, Application US/09479467A
; Patent No. 6723557
; GENERAL INFORMATION:
; APPLICANT: Sternberg, Paul W.
; APPLICANT: Barr, Maureen M.
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE HOMOLOGS REQUIRED FOR MALE MAT
; FILE REFERENCE: BEHAVIOR IN NEMATODES AND ASSAYS BASED THEREON
; FILE REFERENCE: 18021-2501B
; CURRENT APPLICATION NUMBER: US/09/479.467A
; CURRENT FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: 60/115.127
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 2870
; TYPE: PRT
; ORGANISM: C. Elegans Lov-1 sy582 deletion protein
US-09-479-467A-15

Query Match          7.1%; Score 287.5; DB 4; Length 2870;
Best Local Similarity 20.9%; Pred. No. 2e-10;
Matches 214; Conservative 122; Mismatches 349; Indels 339; Gaps 40;
```

QY	2	APGCGSSTAVNSCPSQSLSVLGSFGELAPPKMANITSSQILDQLKAPSLGQFTTTPST	61
Db	306	AMSTSTSTSTSTSTSTTTT---FTSTASTSTSTSTTQ-----QSSSTTSSPSS	354
QY	62	QONSTSHPTTTSWDLKPPTSQSSVLHDLFKSQPEPSPVLSQLSQOQ--QHQSQAATVP	119
Db	355	TTLTSTSTSTSTSTSTSTTTT-----PEITSTLSSLPDNAICSYLDETTT--	390
QY	120	PPGLESPFOAKLRESTPGDSPSTVNKLQLPST-----TIENISVSHOQP	166
Db	391	-----STTTTMTLSTTTTEPSTSTTTTTEVTSTSTTTTTEPTTTTSTASTSTTTPS	445
QY	167	PKHIKLAKRRIIPASKIPASA-----VEMPGSADVTGLNVQGALEFGSEPSLSFGAP	221
Db	446	TSVTSTSPSTSPVTSTVTSSSSSSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST	503
QY	222	SSENSQIPISLYSKSLSEPLNTSLMTSAVQNSYVTSVITSCSLTSSLSNASP----	277
Db	504	SSSSST--PSSSTASSSVSTASTSQSTSQSTST-----TTKSETTSSDGTNPDPYF	555
QY	278	--VAMSSSYDQSSVH-----NRIPYQ-----SPVSS-----SSAP--	306
Db	556	VEKATTFYDSTSVNLTLNSGLGIIGYQTSIECTSPSTSNVSVTYKDGACFTKSVMPRL	615
QY	307	-GT-----IMNGHGGGRSQOQLDTPKT-----TGPPSALPVSLSLPTSTCTAL	349
Db	616	GGTYPASTFVGQNTYFRAWTDDKVVYTYANVYIQEYSSTTIESESSTSAVASSTSS	675
QY	350	LPSTSOHTGDLTSSPLSQLSSLSHQSSLSAHAALSSSTSHTHASVESASHOSQATFS	409
Db	676	TPSTPST--LSTSTVTEPSTRSSDSTSTTSAGSTTLQESTT--TSEESTTDSSTTIS	731
QY	410	TAATSVSSSAS-----SGVSLSSMNTANSCLCGTGCPASASSSSR	450
Db	732	DTSTSTSPSTSTADSTSTLSVDQDFILDGSLSWNETRHEDSINIVLPINAIPTER	791
QY	451	A-----APLVTSGKAPENLPQGVPPPLHNOYLVGPGGLLPA	486
Db	792	SQTFECENVSTEPFLIIKESTCLNYSNTVLNATYSSNIP--IQPI--ETFLVGIGTYEPR	847
QY	487	YPIYGYDELQMLQSLRPVDY-----GI-----PFAAP	514
Db	848	INMTDLTMTQVSHIFTLNVADSTSTSEVTSTTSGSSSSSAISTTSGIESTSTLEAS	907
QY	515	TALASDRSL-----ANNPVGDVTKFG-----RGDSASPAPATTPAQP	553

QY	2	APGCGSSTAVNSCPSQSLSVLGSFGELAPPKMANITSSQILDQLKAPSLGQFTTTPST	61
Db	306	AMSTSTSTSTSTSTSTTTT---FTSTASTSTSTSTTQ-----QSSSTTSSPSS	354
QY	62	QONSTSHPTTTSWDLKPPTSQSSVLHDLFKSQPEPSPVLSQLSQOQ--QHQSQAATVP	119
Db	355	TTLTSTSTSTSTSTSTTTT-----PEITSTLSSLPDNAICSYLDETTT--	390
QY	120	PPGLESPFOAKLRESTPGDSPSTVNKLQLPST-----TIENISVSHOQP	166
Db	391	-----STTTTMTLSTTTTEPSTSTTTTTEVTSTSTTTTTEPTTTTSTASTSTTTPS	445
QY	167	PKHIKLAKRRIIPASKIPASA-----VEMPGSADVTGLNVQGALEFGSEPSLSFGAP	221
Db	446	TSVTSTSPSTSPVTSTVTSSSSSSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST	503
QY	222	SSENSQIPISLYSKSLSEPLNTSLMTSAVQNSYVTSVITSCSLTSSLSNASP----	277
Db	504	SSSSST--PSSSTASSSVSTASTSQSTSQSTST-----TTKSETTSSDGTNPDPYF	555
QY	278	--VAMSSSYDQSSVH-----NRIPYQ-----SPVSS-----SSAP--	306
Db	556	VEKATTFYDSTSVNLTLNSGLGIIGYQTSIECTSPSTSNVSVTYKDGACFTKSVMPRL	615
QY	307	-GT-----IMNGHGGGRSQOQLDTPKT-----TGPPSALPVSLSLPTSTCTAL	349
Db	616	GGTYPASTFVGQNTYFRAWTDDKVVYTYANVYIQEYSSTTIESESSTSAVASSTSS	675
QY	350	LPSTSOHTGDLTSSPLSQLSSLSHQSSLSAHAALSSSTSHTHASVESASHOSQATFS	409
Db	676	TPSTPST--LSTSTVTEPSTRSSDSTSTTSAGSTTLQESTT--TSEESTTDSSTTIS	731
QY	410	TAATSVSSSAS-----SGVSLSSMNTANSCLCGTGCPASASSSSR	450
Db	732	DTSTSTSPSTSTADSTSTLSVDQDFILDGSLSWNETRHEDSINIVLPINAIPTER	791
QY	451	A-----APLVTSGKAPENLPQGVPPPLHNOYLVGPGGLLPA	486
Db	792	SQTFECENVSTEPFLIIKESTCLNYSNTVLNATYSSNIP--IQPI--ETFLVGIGTYEPR	847
QY	487	YPIYGYDELQMLQSLRPVDY-----GI-----PFAAP	514
Db	848	INMTDLTMTQVSHIFTLNVADSTSTSEVTSTTSGSSSSSAISTTSGIESTSTLEAS	907
QY	515	TALASDRSL-----ANNPVGDVTKFG-----RGDSASPAPATTPAQP	553

Db 908 TTDASQDSSTSDSGTSTSDTTSDSSNSTSTSDSGLSQTPDSDSSASDSMTTVD 967
Qy 554 QOSQ-----SQTHTAQPFVNPALP---PGSYTGL-----PY-- 585
Db 968 DASTETPYDLENTWNETVYSENPFYITIPNKEGALTATMCQCRNDSSQPFVLL 1027
Qy 586 -----TGMPSA-FQYGP-TMFVPPASAKQHGVL----- 612
Db 1028 KESNCLTEFGKNGAYSASVSFNPMTSFVPATGTYEFLINVTNRASGESASHIFTMNVVLP 1087
Qy 613 --STPTPPFQOAGVGQHGYSYGYDLDLTQGP-----AAGDYKGGYAGSSQAP 658
Db 1088 TTTTETPP-TTVSSDDAGKGTGTGATCGGTGSGSANTLTSGDAVRTTSGSGSQ 1146
Qy 659 NKSAGSGKGVSVSSSTTGLPDMTGVSYNKTOTFDKQGFHAGTTPPFLPSVLGSGCPL 718
Db 1147 SSTGSGAGSGTTASGSGSGSGSGTGS-----DGVNSGK-----TTALN 1185
Qy 719 ASGAAPGYAPPPFHLHPAHQPHSOLLHHLLPQDAGSGSGQRQSPSS-LQPKQASKPA 777
Db 1186 GDGTGSGTATTPGSHLGDG-----GSTSGSGSDSGSGSVSTKSSGSDT 1230
Qy 778 YGNS 781
Db 1231 SGSS 1234

RESULT 7
US-09-538-092-1081
; Sequence 1081, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 1996-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-12-352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 1081
; LENGTH: 2090
; TYPE: PRF
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P35658

US-09-538-092-1081

Query Match 7.1%; Score 286.5; DB 4; Length 2090;
Best Local Similarity 23.2%; Pred. No. 1.5e-10;
Matches 215; Conservative 104; Mismatches 349; Indels 257; Gaps 43;

Qy 36 ANITSSQILQKAPSLGQFTTTPSTQNSTSHPTTISWD-----LKPPTS 82
Db 965 ASLSRSLQRYEDLDVSSSTSSVSQSESDARTSCDKDEAVVQAPRHAPVVRPFSI 1024
Qy 83 QSSVL-----SHLDFKSP-----EPSPVLSQSRQHQSOQAVT--VPPPG 123
Db 1025 QPSLLHPAAPFAKSHLVHSGSPGVNCTSVATSASKIIPOGADSTMLATKTVKCAPSPSH 1084
Qy 124 E-SPPSQ---AKLRETPGSPSTVNKLLQLPSTTIENISVNHQOPKHKLAKRIPP 179
Db 1085 PISAPQQLAAALRRQASQAPA-VNTLTE---STLXNV-----PQVNVVQELKNP 1132
Qy 180 A-----SKIPASAVEMPGS--ADVTGLNVQFQAL-----EFGSEPSLSEFGSAPSEN 225
Db 1133 ATPSTAMGSSVPYSTAKTPHPVLTPVAANOAKQGLNSLKLPSGTPPASQQLSGSKASG 1192

Qy 226 SNQIPISLYSK-----SLSEPLNLTSLMST-----AVQNSTYTTSTVITSCSLTSSSLNSASP 277
Db 1193 TAKIETAVTSTPSASGQSKPFPSPSGTGNFGIITPTPSNFTAAQAGATPSKESQ 1252
Qy 278 VAMSSSYDQSSVNHRIPIQSPVSSSESAPGTIMHGGGRSQOQLDTPKTTGPPSALPSV 337
Db 1253 DAFSSGGGSRPSVEAIPESPSPSGITSAINT-----TGEPA-----S 1291
Qy 338 SSLPSTTCTALLPSTSOHTGDLTSSPLSOLSSLSHQSSLSAHAAL----- 385
Db 1292 SSRPVAESGIAL--STTSSKLETPPKLCELLPSSLAGETLGSFGLRVQQAODSTKPT 1349
Qy 386 --SSSTS-----HTHASVESASHSQSATFSTAAVS 417
Db 1350 NKASSTSLTSTQPTKTSGVSGFNFTAPPVLKGHKTEPPTSSATTSVA--PPAATSTSS 1407
Qy 418 SASGVSLSMMYANSLCLGTPASASSSSSRRAAPLVTSGKAPPNLP---QGVPPLLHN 474
Db 1408 TAVFGSLPVTASGSGVIFSGGTSLSAGKTSFSGSQQTNSTVPPSAPPTTAATPLPTS 1467
Qy 475 QYLVGPGCLL-----PAYPI-VGYDELOMLQSLRPVDYGYPPAAPALASRDRSLANNP 528
Db 1468 FPTLSFGLSSATTPSLPMSAGRSTEEATSSALPEKPGDSEVSASASLLEEQSAQLP 1527
Qy 529 YPGDVTKFGSGDSASPAPATTTPAQPOQSQSTHHTAQPPFVNPALPPGYSYTGLPYYTGM 588
Db 1528 QAPPQT-----SDSVKKEPVL--AQPAVNSGTAASSTSLV-----ALSAEATPATTV 1574
Qy 589 PSAPQYQPTMFVPPASA-----KQGVNL-----STPTP-----PFQ 620
Db 1575 PDA-----RTEAVPPASSFVPGQTAVTAAAISSAGPVAVETSTPTIASSTTSIVAPGPSA 1630
Qy 621 QASGYG-----QHGYSTGYDDLTQCTAACDYSKG--GYAGSSQAPNKSAGSG 665
Db 1631 EAAAFGTVTSGSVFAOPPAASSSSAFNQNTNNTATAPSATPVFQVAASTPS--LFGQQ 1689
Qy 666 PGKGVSVSSSTTGLPDMTGSVYNNKTQTFDKQGHAGTTPPPF--SLPSVLAST----- 715
Db 1690 TGSTASTAAAT--PQVSSS-----GF---SSPAFGTTAPGVFGOTTFGQASVF 1732
Qy 716 GPLASGAAP--GYAPPPFHLHPAHQPHSOLLHHLLPQDQAQSGS--GQRSQPSLSQPKS 771
Db 1733 GQSASSAASVFSFQPGFSSV-PAFGQPASS-----TPTSTSGSVFGAASSTSSSSSFS 1785
Qy 772 -----QASKPAYGNP 782
Db 1786 FGSSPNTGGGLFGQSNAPAFQSP 1810

RESULT 8

US-09-134-001C-4463
; Sequence 4463, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4463
; LENGTH: 2137
; TYPE: PRF
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4463

Query Match 7.0%; Score 282.5; DB 3; Length 2137;

Qy	670	VVSSTTGTPDMVTGSVYNKTKQTDFDKGFGHAGTTPPFSLPSVLGSGTGPLASGAAPGVAPP	729
Db	1687	PAAAQTLLALAP-----ASTQSPASQASSLVVS---ASGAAP--LPV	1722
Qy	730	PFLHILPAHQPHSQLLHHHLPDQASGSGORSQSPSSIQ-----PKSQASKPAYGNSPYW	784
Db	1723	TWVSRLPVSKDE-----PDTLURSPPSPSPSTATSGGRRPRRQPPPPRSPFY	1772
RESULT 11			
US-09-248-796A-17307			
; Sequence 17307, Application US/09248796A			
; Patent No. 6747137			
; GENERAL INFORMATION:			
; APPLICANT: Keith Weinstock et al			
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDID			
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS			
; FILE REFERENCE: 107196.132			
; CURRENT APPLICATION NUMBER: US/09/248,796A			
; CURRENT FILING DATE: 1999-02-12			
; PRIOR APPLICATION NUMBER: US 60/074,725			
; PRIOR FILING DATE: 1998-02-13			
; PRIOR APPLICATION NUMBER: US 60/096,409			
; PRIOR FILING DATE: 1998-08-13			
; NUMBER OF SEQ ID NOS: 28208			
; SEQ ID NO 17307			
; LENGTH: 827			
; TYPE: PRT			
; ORGANISM: Candida albicans			
US-09-248-796A-17307			
Query Match 6.6%; Score 269; DB 4; Length 827;			
Best Local Similarity 22.5%; Pred. No. 6.5e-10;			
Matches 171; Conservative 102; Mismatches 314; Indels 174; Gaps			
Qy	20	SSVLGSGFGLAPPKMANITSSQILDQLKAPSLGQFTTTPSTQONSTGSHPTTTTSDWLKP	79
Db	56	NSIFGNDNLVNOPSTNGATSTGHFFGPSIPSTSTHOCTPGETSNVYN--TKSSSQNSQP	113
Qy	80	PTSQSSVLSHLDFKSGQPEPSPV-----LSQLSQRQHQSOAVTVPPGLSFPQSQAKLRE	134
Db	114	STSPSTVAAAATSS---SPVASTRPASTSQQEEASTARQSTSPATTATNTPTPSP	170
Qy	135	STPGDSP-----STVNKLQLPSTTTIENISVSVHQPQPKHIAKARRIPPASKIPASA	187
Db	171	STSKETPTNTAQTTSSANNQSSNTAAP--STSVIOPSTSEVHVQSQQTSTTPNTPTSS	228
Qy	188	VEMPGSADVTGLNVQFALFEGSEPSLSEFGSAPSSENSNOIPISLYSKLSLSEPLNTLS	247
Db	229	PNTPTTSE-----AAPTTSAPTTEAPVTPST--SEWVP---NTPTTSEAPNTPTT	275
Qy	248	MTSAVQNSTYTTSVITSCSLTSSSLN---SASPVMSSSYDQSSVHNRIYPQSPV--SS	301
Db	276	SEAPVTPS--TSEVVPNTPTSKAPNTPTSEAPATPTTS---EAPNTPTTSEAPVTPTT	330
Qy	302	SEAGPTGMKHGGGRS-----QOTLDTPKTTGPP-----SALPSVSLPSTTSCIAL	349
Db	331	SEVVPPTSTOGDAVSSTSVTSGTTLTSSLLPPTTALTQTSTPEASDPKPSSTISIE	390
Qy	350	LPSTSOHTGD-----LTSPLSQSSLSLSSHQSLSHAHAALSSSTSTHT	392
Db	391	TPSTSTEQPTTTTSSVGPSPSEBQPTTTSELAVTNSPQBSTSLVEPTTSSLESNT	450
Qy	393	HASVESASSHQSNATFTSTAATSVSSSASSGVSLSSSNNTANSILCLGCTPASA-----	444
Db	451	PTPNPSTSEAPQSTASQADPDPTTSSAPA--PELSSSNADPESNLVLHSSSTSLTNPTDSQ	509
Qy	445	--SSSSSRAAPLVTSGKAPNLPQGVPLLNQYLVGPGGLLPAYPIYGYDELQMLQSLR	502
Db	510	IDSSSTTDAVSQATTEPTSENTTAASSVTAN-----	541
Qy	503	PVDYVYGIFFAAPALAS-----RDRSLANNPIPGDVTTKFGSGSASAPATP-----	548

Db	1130	IQSEV--TVPTBEGIAGVATSTGVTSG-----GLPIPPVSESPVLSSVVSSITIPA	1179
Qy	337	VSLPSTT-----SCTALLPS-----TSQHTGDLTSP-----	364
Db	1180	VWSITSTPSLQVPTSTSEIVSSSTALYPSVTVSATSAGGSTATPGPKPPAVVSQAA	1239
Qy	365	-----LSQLSSSLSSHQSLSAHAALSSSTSH--THASVESA-----SHQSATSATF	408
Db	1240	GSTTVGANTLTSVSTTTSPFSTASQLSLSLSSTSTPTLAEVTVVSAHSLDKTSHSSTTGL	1299
Qy	409	STAATSVSSASGVSLSSSMNTANSL-----CLGGTPASASSSSRAAPLVTS--GKA	460
Db	1300	AFSLSAPSSSSPCAGVSSYISQPGGLHPLVPSVIASTPILPQAGTPTPLLPQVPSI	1359
Qy	461	PP-----NLPGQVPPLLNQYLVGPGGILPAYP-----IYGYDELOMLQS	500
Db	1360	PPLVQPVANVPVQOTLIHSQ---PQALLPNQPHTHCPVEDSDTQPKAPGIDDIKTL	1416
Qy	501	RLPVDYY-----GIP--FAAPTALASRDRSLANNPYPGD	532
Db	1417	KLRSLPSEHSSGQAQHASVLSLETSLVTESTVTGPIPTTAVAPSKLLTSTTCLUPP	1472
Qy	533	VTKEGRGDSAP-APATTAPQPOQSQTHHTAQOPFVNPALPPGYSYVTLGPLYTGMPSA	591
Db	1473	-TNLPLGTVALPVTVPVTPQGVSTPVSTT--TSGVKPGTAFSPKPLTKAPVLPGVTELPAG	1530
Qy	592	FQYQPTMFVPPASAKQHGVLNSTPTPPFQOASGVQGHGYSTGYDDLLTQGTAAGYSGGY	651
Db	1531	TL--PSEQLPFP--GPSLTQSQPLEDIDAQLRRTLSP--EXITVTSAVGPVSM--	1580
Qy	652	AGSSQAPN--KSAGSGRGKGV-----VSSSTTGLPDM-----TGSVY	687
Db	1581	-----APTATTEAGTQPKGVSVQKEGPVLATSSGAVFKRGRFQVSVAADGAQKEG--	1633
Qy	688	NKTOTFDKQGHAGTTPPFSLPSVLGSTGTPASGAAPGYAPPFLHILPAHQHQSLLH	747
Db	1634	NKSEDAKSVHESST----SESSVLSSSSPESTLV---KPEPNGITIPGISSDVPESA	1689
Qy	748	HHLPDQAQSGSQRSQPSLSQPKQASK	775
Db	1686	KTTASEAKSDTQPTKVGRFQVTTTANK	1713

```

RESULT 13
US-09-854-856-42
; Sequence 42, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 2032
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2032)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-42

Query Match          6.4%; Score 260.5; DB 4; Length 2032;
Best Local Similarity 20.6%; Pred. No. 8.5e-09;

```

```

542  --DINSAQYSAPTSNADAETAASSPVSEQLATGSGTSLDTTAGASSTPASEATANIESTFG 599
549  TPAQPOQSQS---QTHHTTAQPFNPA-----LPPGVSYTGLPYVTGMPSAFQ--- 593
600  TDGSDASQATTAETTSPPDOSVVTPSASAPDVSTLPTG-SESGTSLVSGSETSIDTNT 658
594  --YGTMFVPASAKQHGVNLSSTPPFPQASGYGQHGYSTGYDDLTQGTAAGDYKGGY 651
659  VASGSTV-IPSS-----NIPTQSP-----SQSVVSSDAASNV 691
652  AGSQAPNKSAGSGFGKGVSVSSSTTGLPD-MTGSVYNKTQ 691
692  STGSATTDLAGSETGV-QPISSSATGTSEPVFSSEYNSS 731

RESULT 12
US-09-854-856-58
; Sequence 58, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 2004
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2004)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-58

```

```

Query Match      6.4%; Score 260.5; DB 4; Length 2004;
Best Local Similarity 20.6%; Pred. No. 8.3e-09;
Matches 204; Conservative 141; Mismatches 370; Indels 273; Gaps 43;

QY      2  APGTGSGTAV-----NSCPSQSSVLVSGSGFGLAPPKM---AN 37
      |||  |||
Db      785  APTTSSQOAVLESTQGSQVAPAEFVAQOQATQPTTLASSVDASHDVASGMSDGNEN 844
      |||  |||

QY      38  ITSS-----QILDOLKAPSLGQFTTP-----STQQNSTSHPTT 71
      |||  |||
Db      845  VPSGSRHEGHTTKRHKRYSVRSSRHEKTSRPKLRLNVSNKGDVRVCEQLETHNRKMV 904
      |||  |||

QY      72  TTSDWL--KPTSSQSSVLSHLDKFSQPESPVLSQ---LSRQQHQSQAVTVPP---PG 122
      |||  |||
Db      905  TKFDLDGDNPEETATIMVNDNFILATERESFVDQVREIIEKADEMLSDVSVPEGDOG 964
      |||  |||

QY      123  LES-----FPGQAKLRETPGDSP-STVNKLLQLPSTTIENISVS-----VHQPQPK 168
      |||  |||
Db      965  LESLQGDYDYGSGSQLEGEFKQPIPASSMPOQIGPISLTQVHSGARRFIVSPVPE 1024
      |||  |||

QY      169  HTKLAKRIPPA---SKTPASAVEMPGSADVTGLNVQFGALEFCGSEPSLGEFGSATSSEN 225
      |||  |||
Db      1025  S-RLRESKVFPFSEITDVTAAATOSP-----GMNLSHSASLSLQQAQFELRAQWTEG 1077
      |||  |||

QY      226  SNQIPISLYSKLSSEP-LNTLSLMTSAVQNSTYTTTTSVITSCSLTSSSLNSASVPVAMSSSY 284
      |||  |||
Db      1078  PNTAPPNFSHTGPTFPVVPFPFLSSITAGVPTTAATAPVA-----TSSPPNDISTSV 1129
      |||  |||

QY      285  DOSSVHNRIPOYPSSVSSSESAPGTIMNGHGGRSQOITLDTPTKTTGPP-----SALPS 336
      |||  |||

```

```
Matches 204; Conservative 141; Mismatches 370; Indels 273; Gaps 43;
Qy 2 APGTGSSTAV-----NSCSPQSLSSVLGSGFGLAPPKM---AN 37
Db 813 APTTSSQAVLESTQGVSOVAPAEVPAVQAQPTTTLASSVDSAHSDVASGMSDGNEN 872
Qy 38 ITSS-----QILDQLKAPSLGQFTTTP-----STQONSTSHPTT 71
Db 873 VPSSGRHEGRTTKRHYKSVRSRHEKTSRPLKRLNVSNKGDVVECCLETHNRKVV 932
Qy 72 TTSWDL--KPTSSQSVSLHDLDFKSPSPVLSQ----LSQROHQSOQAVTVP---PG 122
Db 933 TFKFDLGDGNPEEATITMWNDFILAIERESFVDQVREIIEKADEMUSEDVSVPEGDOG 992
Qy 123 LES-----FPSQAKLRESTPGDSP--STVNKLILQLPSTTIENISVS-----VHQPOPK 168
Db 993 LESLQGDYDGFSGSKLEGEFKQIPASSMPQIQIGTSSLTQVHVSAGRFFIVSPVPE 1052
Qy 169 HIKLAKRIPPA---SKIPASAVEMPGSADVTGLNVQFGLFEGFSEPSLSEFGSAPSEN 225
Db 1053 S-RLRESKVFPSEITDTVAATAQSP-----GMNLSHSASSLSLQQAFAFSELRAQMTEG 1105
Qy 226 SNQIPISLYSKLSEP--LNTSLMTSAVQNSTYTTVITSCSLTSSLSNASPVAMSSSY 284
Db 1106 PNTAPPNFSHTGTPFPVPPFLSSITAGVPTTAAATAPVPA-----TSSPPNDISTSV 1157
Qy 285 DQSSVHNRIQSPVSSSESAPGTIMNGHGGRSQOITLDTPTKTGPP-----SALPS 336
Db 1158 IQSEV--TVPTTEGIAGVATSTGVVTSG-----GLPIPVSESPVLSVSVSSIIIPA 1207
Qy 337 VSSLPSTT-----SCTALLPS-----TSQHTGDLTSSP----- 364
Db 1208 VVSIITSPSLQVPTSTSEIVVSTALYPSVTVSATSASAGGSTATPGKPPAVVSOQAA 1267
Qy 365 -----LSQLSLSSSHQSSLSAHLSSSTSH---THASVESA-----SSHQSATP 408
Db 1268 GSTTVGATLTSVSTTTPSTASQLSITLSSSTSTPTLAETVTVVSAHSLDKTSHSTGL 1327
Qy 409 STAATSVSSSASSGVSSSSMNTANSL-----CLGTPASASSSSRAAPLVTS--GKA 460
Db 1328 AFSLAPSSSSSPGAGVSSYISQPGGLHPLVPSVIASPTLPQAGTSTFLLPQVPSI 1387
Qy 461 PP-----NLPQGVPPLLHNQYLVGPGGLPAYP-----IYGYDELOMLQS 500
Db 1388 PPLVQPVANVPAVQOTLIHSQ---POPALLPNQPHTHCPEVDSDTQPKAPGIDDIKLEE 1444
Qy 501 RLPVDY-----GIP--FAAPTALASDRSLANNPYPGD 532
Db 1445 KRLSLESHSSGQASHVSLETSLVISTVTPGIPPTTAVAPSKLLTSTTCLPP--- 1500
Qy 533 VTKEGRGDSASP-APATTAPQOQSQTHHTAQOPFVNAPALPGYSVTGLPYVTGMPSA 591
Db 1501 -TNPLGTVALPVTVPTGQVSTPVSTT--TSQVKPGTAPSKPLTKAPVLVPGTELPA 1558
Qy 592 FOYGTFMVPVPAQAKHGVLNSTPTPPFPQASGYGQHGYSTGYDDLTGTAAGDYSGGY 651
Db 1559 TL--PSEQLPFP---GPSLTQSOQPLEDLDAQLRLTSLP--EXITVTSVAVGPVMA-- 1608
Qy 652 AGSSQAPN--KSAGSGPKGVSS-----VSSSTTGLPDM-----TGSVY 687
Db 1609 -----APTAITEAGTQPKGVSVQKEGFPVLATSSGAGVFKMRFPQVSAADGAQKEG-- 1661
Qy 688 NKTOTFDKQGHACTPPPPFSLPSVLGSTGTPLASGAAFCYAPPPPLHLPAHQPHSOLLH 747
Db 1662 NKSEDAKSVHEST-----SESSVLSSSSPESTLV-----KPEPNGITIPGISSVDVPESAH 1713
Qy 748 HHLPQDAQSGSGQSPQSLQPKSQAK 775
Db 1714 KTTASEAKSDTGFTKVRFGVTTTANK 1741
```

RESULT 14

US-09-854-856-26

```
; Sequence 26, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 2064
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2064)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-09-854-856-26
```

```
Query Match 6.4%; Score 260.5; DB 4; Length 2064;
Best Local Similarity 20.6%; Pred. No. 8.6e-09;
Matches 204; Conservative 141; Mismatches 370; Indels 273; Gaps 43;
```

```
Qy 2 APGTGSSTAV-----NSCSPQSLSSVLGSGFGLAPPKM---AN 37
Db 845 APTTSSQAVLESTQGVSOVAPAEVPAVQAQPTTTLASSVDSAHSDVASGMSDGNEN 904
Qy 38 ITSS-----QILDQLKAPSLGQFTTTP-----STQONSTSHPTT 71
Db 905 VPSSGRHEGRTTKRHYKSVRSRHEKTSRPLKRLNVSNKGDVVECCLETHNRKVV 964
Qy 72 TTSWDL--KPTSSQSVSLHDLDFKSPSPVLSQ----LSQROHQSOQAVTVP---PG 122
Db 965 TFKFDLGDGNPEEATITMWNDFILAIERESFVDQVREIIEKADEMUSEDVSVPEGDOG 1024
Qy 123 LES-----FPSQAKLRESTPGDSP--STVNKLILQLPSTTIENISVS-----VHQPOPK 168
Db 1025 LESLQGDYDGFSGSKLEGEFKQIPASSMPQIQIGTSSLTQVHVSAGRFFIVSPVPE 1084
Qy 169 HIKLAKRIPPA---SKIPASAVEMPGSADVTGLNVQFGLFEGFSEPSLSEFGSAPSEN 225
Db 1085 S-RLRESKVFPSEITDTVAATAQSP-----GMNLSHSASSLSLQQAFAFSELRAQMTEG 1137
Qy 226 SNQIPISLYSKLSEP--LNTSLMTSAVQNSTYTTVITSCSLTSSLSNASPVAMSSSY 284
Db 1138 PNTAPPNFSHTGTPFPVPPFLSSITAGVPTTAAATAPVPA-----TSSPPNDISTSV 1189
Qy 285 DQSSVHNRIQSPVSSSESAPGTIMNGHGGRSQOITLDTPTKTGPP-----SALPS 336
Db 1190 IQSEV--TVPTTEGIAGVATSTGVVTSG-----GLPIPVSESPVLSVSVSSIIIPA 1239
Qy 337 VSSLPSTT-----SCTALLPS-----TSQHTGDLTSSP----- 364
Db 1240 VVSIITSPSLQVPTSTSEIVVSTALYPSVTVSATSASAGGSTATPGKPPAVVSOQAA 1299
Qy 365 -----LSQLSLSSSHQSSLSAHLSSSTSH---THASVESA-----SSHQSATP 408
Db 1300 GSTTVGATLTSVSTTTPSTASQLSITLSSSTSTPTLAETVTVVSAHSLDKTSHSTGL 1359
Qy 409 STAATSVSSSASSGVSSSSMNTANSL-----CLGTPASASSSSRAAPLVTS--GKA 460
Db 1360 AFSLAPSSSSSPGAGVSSYISQPGGLHPLVPSVIASPTLPQAGTSTFLLPQVPSI 1419
Qy 461 PP-----NLPQGVPPLLHNQYLVGPGGLPAYP-----IYGYDELOMLQS 500
Db 1420 PPLVQPVANVPAVQOTLIHSQ---POPALLPNQPHTHCPEVDSDTQPKAPGIDDIKLEE 1476
```

```
QY 501 RLPVDY-----GIP--FAAPTALASDRSLANNPYPGD 532
Db 1477 KLSLSEHSSGAQHASVLETSLSLVTGPTTAVAPSKLLTSTTCLPP----- 1532
QY 533 VTKFGRGDSASP-APATTAPQOQSQTHHTAQOPFVNPPALPGYSYTGLPYTGMPSA 591
Db 1533 -TNLPLGTVALPVTVPVTPQGVSTPVT--TSGVKFGTAPSKPPLTKAPVLEPGTCLPAG 1590
QY 592 FOYGTMTFVPASAKOHGYNLSTPTPPFOQASGYQHGYSTGYDDLTOGTAAGDYSKGGY 651
Db 1591 TL--PSEQLPFPF-----GSLTOSQOPLDLDLQALRTLSL--EXITVTSAGVPVMA-- 1640
QY 652 AGSSQAPN--KSAGSGPKGVS-----VSSSTTGLPDM-----TGSVY 687
Db 1641 -----APTAITEAGTQPKGVSVKSGVPLATSSGAGVFKMGRFQVSAADGAQKEGK-- 1693
QY 688 NKTQTFDKQGFHAGTTPPFLPSVLSTGTLASGAAPGYAPPFLHILPAHQPHSOLLH 747
Db 1694 NKSEDAKSVHFESST-----SESVLSSSPESTLV-----KPEPNGITIPGISDVPESA 1745
QY 748 HHLPODAQSGGORSQPSLSQPKSOASK 775
Db 1746 KTTASEAKSDTGQPTKVGRFQVTTTANK 1773

RESULT 15
US-09-854-856-10
; Sequence 10, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; FILE REFERENCE: Encoding the Same
; CURRENT FILING DATE: 2001-05-14
; PRIOR FILING DATE: 2001-05-14
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 2092
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2092)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-10
```

```
Query Match 6.4%; Score 260.5; DB 4; Length 2092;
Best Local Similarity 20.6%; Pred No. 8.8e-09;
Matches 204; Conservative 141; Mismatches 370; Indels 273; Gaps 43;

QY 2 APGTGSSTAV-----NCSQPSQSLSVLGGFGELAPPKM---AN 37
Db 873 APTTSSQAVLESTQGVSAPEAVPAVQAPOATQPTTLASSVDSAHSDVASGMSDGNEN 932
QY 38 ITSS-----QILDQKAPSLGQPTTTP-----STQONSSTHPTT 71
Db 933 VPSSSGRHEGRTTKRHYKRSVRSRHEKTSRPKRLNVNKGDRVVECCOLETHNRKOV 992
QY 72 TTSWDL--KPTTSQSVLGHDFKXQPEPSVLQ-----LSRQOQHQSOAVTVP--PG 122
Db 993 TKFEDLDGNPEIATIMVNDLAIERESFDQVREIIEKADEMLSEDSVSEPEGQOG 1052
QY 123 LES-----FPSQAKLRESTPGDSP-STVNKLLQLPSTTIENISVS-----VHQPOPK 168
Db 1053 LESLQKDDYGFSGSKLEGEFKQIPASSMPPQOIGIPTSSLTQVHSGRRFIVSPVPE 1112
```

```
QY 169 HIKLAKERIPPA---SKIPASAVEMFGSADVTGLNVQFGLIEFGSEPSLSEFGSAPSEN 225
Db 1113 S-RURESKVPSEITDVTAASTAQSP-----GMNLSHSASSLSLQOAFSELRRQWTEG 1165
QY 226 SNOITPISLYSKSLSEP-LNTSLNMTSAVQNSTTTTTSVITSCSLTSSLSNLSASVPANSSSY 284
Db 1166 PNTAPPNFSHTGPTFPVPPFLSIAGVPTTAAATAFVPA-----TSSPNNDISTSV 1217
QY 285 DQSVNHRIPYQSPVSESSESAPGTINMGHGGRSQOQTLDPKTKTTPP-----SALPS 336
Db 1218 IQSEV--TVPTIEGIAGVATSTGVVTSG-----GLPIPPVSESPVLSSVVSSITIPA 1267
QY 337 VSSLPSTT-----SCTALLPS-----TSQHTGDLTSSP----- 364
Db 1268 VSISTSPSLQVPTSTSEIIVSSTALYPSVTSASAGGSTATPGKPPPAVVSQAA 1327
QY 365 -----LSQSSLSHSHOSSLSAHAALSSSTSH-----THASVESA-----SSHQSATF 408
Db 1328 GSTTVGATLTSVSTTSPFPSTASQSLSTSTPTLAETVVVSAHSLDKTSHSSTGL 1387
QY 409 STAATSVSSSASSGVSLSMNTANSL-----CLGCTPASASSSSSSRAAPLVS--GKA 460
Db 1388 AFSLSAPSSSSSGAGVSSYISQGLHPLVPSVIASTPILPOAGTSTPCLLPQVPSI 1447
QY 461 PP-----NLPQGVPPPLHNOYLVPQGLLPAYP-----IYGYDELOMLQS 500
Db 1448 PPLVQPVANVPAVQTLHSQ---PQALLPNQPHTHCPVDSDTQPKAFGIDDIKTEE 1504
QY 501 RLPVDY-----GIP--FAAPTALASDRSLANNPYPGD 532
Db 1505 KLSLSEHSSGAQHASVLETSLSLVTGPTTAVAPSKLLTSTTCLPP----- 1560
QY 533 VTKFGRGDSASP-APATTAPQOQSQTHHTAQOPFVNPPALPGYSYTGLPYTGMPSA 591
Db 1561 -TNLPLGTVALPVTVPVTPQGVSTPVT--TSGVKFGTAPSKPPLTKAPVLEPGTCLPAG 1618
QY 592 FOYGTMTFVPASAKOHGYNLSTPTPPFOQASGYQHGYSTGYDDLTOGTAAGDYSKGGY 651
Db 1619 TL--PSEQLPFPF-----GSLTOSQOPLDLDLQALRTLSL--EXITVTSAGVPVMA-- 1668
QY 652 AGSSQAPN--KSAGSGPKGVS-----VSSSTTGLPDM-----TGSVY 687
Db 1669 -----APTAITEAGTQPKGVSVKSGVPLATSSGAGVFKMGRFQVSAADGAQKEGK-- 1721
QY 688 NKTQTFDKQGFHAGTTPPFLPSVLSTGTLASGAAPGYAPPFLHILPAHQPHSOLLH 747
Db 1722 NKSEDAKSVHFESST-----SESVLSSSPESTLV-----KPEPNGITIPGISDVPESA 1773
QY 748 HHLPODAQSGGORSQPSLSQPKSOASK 775
Db 1774 KTTASEAKSDTGQPTKVGRFQVTTTANK 1801
```

Search completed: January 31, 2005, 17:47:58
Job time : 29 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 31, 2005, 17:42:12 ; Search time 71 Seconds
(without alignments)
3999.626 Million cell updates/sec

Title: US-10-509-307-1

Perfect score: 4055

Sequence: 1 MAPGTGSSAVNSCSQSLSS.....LQPKSQASKPAYGNSPYWTN 786

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/FCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/FCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1536	37.9	363	10	US-09-946-374-72
2	1536	37.9	363	13	US-10-052-586-252
3	1536	37.9	363	14	US-10-174-590-252
4	1536	37.9	363	14	US-10-176-758-252
5	1536	37.9	363	14	US-10-175-737-252
6	1536	37.9	363	14	US-10-174-581-252
7	1536	37.9	363	14	US-10-176-483-252
8	1536	37.9	363	14	US-10-176-483-252
9	1536	37.9	363	14	US-10-176-914-252
10	1536	37.9	363	14	US-10-176-915-252
11	1536	37.9	363	14	US-10-173-706-252
12	1536	37.9	363	14	US-10-175-738-252
13	1536	37.9	363	14	US-10-175-752-252

14	1536	37.9	363	14	US-10-176-482-252	Sequence 252, App
15	1536	37.9	363	14	US-10-176-757-252	Sequence 252, App
16	1536	37.9	363	14	US-10-176-913-252	Sequence 252, App
17	1536	37.9	363	14	US-10-180-552-252	Sequence 252, App
18	1536	37.9	363	14	US-10-180-557-252	Sequence 252, App
19	1536	37.9	363	14	US-10-173-700-252	Sequence 252, App
20	1536	37.9	363	14	US-10-174-572-252	Sequence 252, App
21	1536	37.9	363	14	US-10-174-579-252	Sequence 252, App
22	1536	37.9	363	14	US-10-174-582-252	Sequence 252, App
23	1536	37.9	363	14	US-10-174-588-252	Sequence 252, App
24	1536	37.9	363	14	US-10-175-739-252	Sequence 252, App
25	1536	37.9	363	14	US-10-175-740-252	Sequence 252, App
26	1536	37.9	363	14	US-10-175-743-252	Sequence 252, App
27	1536	37.9	363	14	US-10-176-488-252	Sequence 252, App
28	1536	37.9	363	14	US-10-176-492-252	Sequence 252, App
29	1536	37.9	363	14	US-10-176-747-252	Sequence 252, App
30	1536	37.9	363	14	US-10-176-750-252	Sequence 252, App
31	1536	37.9	363	14	US-10-176-985-252	Sequence 252, App
32	1536	37.9	363	14	US-10-176-987-252	Sequence 252, App
33	1536	37.9	363	14	US-10-176-992-252	Sequence 252, App
34	1536	37.9	363	14	US-10-176-993-252	Sequence 252, App
35	1536	37.9	363	14	US-10-184-658-252	Sequence 252, App
36	1536	37.9	363	14	US-10-176-991-252	Sequence 252, App
37	1536	37.9	363	14	US-10-173-695-252	Sequence 252, App
38	1536	37.9	363	14	US-10-173-697-252	Sequence 252, App
39	1536	37.9	363	14	US-10-173-705-252	Sequence 252, App
40	1536	37.9	363	14	US-10-174-576-252	Sequence 252, App
41	1536	37.9	363	14	US-10-174-585-252	Sequence 252, App
42	1536	37.9	363	14	US-10-174-586-252	Sequence 252, App
43	1536	37.9	363	14	US-10-175-747-252	Sequence 252, App
44	1536	37.9	363	14	US-10-176-481-252	Sequence 252, App
45	1536	37.9	363	14	US-10-176-485-252	Sequence 252, App

ALIGNMENTS

RESULT 1
US-09-946-374-72
; Sequence 72, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946.374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749

us-10-509-307-1.rapb


```
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

Query Match      37.9%; Score 1536; DB 10; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 7 SSTAVNSCS--PQSLSSVLGSGFELAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 64
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
9 NSVLLRICPSFPLLKSSVLGSGFELAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 68

Qy 65 STSHPTTTTNDLKPPTSQSSVLHLDPKSPVLSQSQHQHQSQAVTVPPFGL 124
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
69 STSHPTTTTNDLKPPTSQSSVLHLDPKSPVLSQSQHQHQSQAVTVPPFGL 128

Qy 125 SFPQAKLRSTPGDPSVTNKLQLPSTTTTENSVSHPQPKHIKLAKRIPPASKIP 184
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
129 SFPQAKLRSTPGDPSVTNKLQLPSTTTTENSVSHPQPKHIKLAKRIPPASKIP 188

Qy 185 ASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSPSSSENSNOIPISLYSKSLSEPLNT 244
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
189 ASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSPSSSENSNOIPISLYSKSLSEPLNT 248

Qy 245 SLSMTSAVONSTYTTTTSLSLSSSLNSASPVAMSSSYDQSSVHNRIPQSPVSSSES 304
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
249 SLSMTSAVONSTYTTTTSLSLSSSLNSASPVAMSSSYDQSSVHNRIPQSPVSSSES 308

Qy 305 APGTIMNGHGGRSQOQLDT 324
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
309 APGTIMNGHGGRSQOQLDLS 328

RESULT 2
US-10-552-586-252
; Sequence 252, Application US/10052586
; Publication No. US20020127584A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/052,586
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
```

```

; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086486
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087098
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087208
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088722
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR APPLICATION NUMBER: 60/089908

Query Match          37.9%; Score 1536; DB 13; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 7 SSTAVNSCS--PQSLSSVLGSGFGLAPPKMANITSSQILDOLKAPSLGQTTTPTSTQON 64
DB 9 NSVILRICSFIPLLKSSVLGSGFGLAPPKMANITSSQILDOLKAPSLGQTTTPTSTQON 68
QY 65 STSHPTTTTSDWKPTTSQSSVLSHLDKSPSPVLSQLSORQOHSQAVTVPPGLE 124
DB 69 STSHPTTTTSDWKPTTSQSSVLSHLDKSPSPVLSQLSORQOHSQAVTVPPGLE 128
QY 125 SPFSQAKLRSTPGDSPSTVNKLLQLPSTTIENISVSVHQPOPKHKLAKRRIPPASKIP 184
DB 129 SPFSQAKLRSTPGDSPSTVNKLLQLPSTTIENISVSVHQPOPKHKLAKRRIPPASKIP 188
QY 185 ASAVEMPGSADVTGLNVQFGLPEGSEPSLSFEGSAPSESENQIPISTYKSLSEPLNT 244
DB 189 ASAVEMPGSADVTGLNVQFGLPEGSEPSLSFEGSAPSESENQIPISTYKSLSEPLNT 248
QY 245 SLSTSAVQNSTYTTSTVITSSCSLTSSLSNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSES 304
DB 249 SLSTSAVQNSTYTTSTVITSSCSLTSSLSNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSES 308
QY 305 APGTIMNGHGGGRSQOQLD 324
DB 309 APGTIMNGHGGGRSQOQLD 328

RESULT 3
US-10-174-590-252
; Sequence 252, Application US/10174590
; Publication No. US2003008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; PRIOR APPLICATION NUMBER: 60/088722
; PRIOR FILING DATE: 1998-06-10
```

```
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C42
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-590-252

Query Match      37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 7 SSTAVNSCS--POSLSVLGSGFGELAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 64
Db 9 NSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 68
Qy 65 STSHPTTTTSDWLKPPPTSSQSVLSHLDFKQPEPSVLSQSRQHQSOAVTVPPPGLE 124
Db 69 STSHPTTTTSDWLKPPPTSSQSVLSHLDFKQPEPSVLSQSRQHQSOAVTVPPPGLE 128
Qy 125 SPPSOAKLRESTPGDSPSTVTKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIIPPASKIP 184
Db 129 SPPSOAKLRESTPGDSPSTVTKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIIPPASKIP 188
Qy 185 ASAVEMPGSADVTGLNVQFGLGFEPSLSSEFGSAPSSSENSNOIPISLSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLGFEPSLSSEFGSAPSSSENSNOIPISLSKSLSEPLNT 248
Qy 245 SLSMTSAVQNSTYTTSVITSCSLTSSLSNLSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 304
Db 249 SLSMTSAVQNSTYTTSVITSCSLTSSLSNLSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 308
Qy 305 APGTIMNGHGGGRSQOQLD 324
Db 309 APGTIMNGHGGGRSQOQLD 328

RESULT 4
US-10-176-758-252
; Sequence 252, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-252

Query Match      37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 7 SSTAVNSCS--POSLSVLGSGFGELAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 64
Db 9 NSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 68
Qy 65 STSHPTTTTSDWLKPPPTSSQSVLSHLDFKQPEPSVLSQSRQHQSOAVTVPPPGLE 124
Db 69 STSHPTTTTSDWLKPPPTSSQSVLSHLDFKQPEPSVLSQSRQHQSOAVTVPPPGLE 128
Qy 125 SPPSOAKLRESTPGDSPSTVTKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIIPPASKIP 184
Db 129 SPPSOAKLRESTPGDSPSTVTKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIIPPASKIP 188
Qy 185 ASAVEMPGSADVTGLNVQFGLGFEPSLSSEFGSAPSSSENSNOIPISLSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLGFEPSLSSEFGSAPSSSENSNOIPISLSKSLSEPLNT 248
Qy 245 SLSMTSAVQNSTYTTSVITSCSLTSSLSNLSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 304
Db 249 SLSMTSAVQNSTYTTSVITSCSLTSSLSNLSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 308
Qy 305 APGTIMNGHGGGRSQOQLD 324
Db 309 APGTIMNGHGGGRSQOQLD 328

RESULT 5
US-10-175-737-252
; Sequence 252, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-252

Query Match      37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 7 SSTAVNSCS--POSLSVLGSGFGELAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 64
Db 9 NSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 68
Qy 65 STSHPTTTTSDWLKPPPTSSQSVLSHLDFKQPEPSVLSQSRQHQSOAVTVPPPGLE 124
Db 69 STSHPTTTTSDWLKPPPTSSQSVLSHLDFKQPEPSVLSQSRQHQSOAVTVPPPGLE 128
Qy 125 SPPSOAKLRESTPGDSPSTVTKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIIPPASKIP 184
Db 129 SPPSOAKLRESTPGDSPSTVTKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIIPPASKIP 188
Qy 185 ASAVEMPGSADVTGLNVQFGLGFEPSLSSEFGSAPSSSENSNOIPISLSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLGFEPSLSSEFGSAPSSSENSNOIPISLSKSLSEPLNT 248
Qy 245 SLSMTSAVQNSTYTTSVITSCSLTSSLSNLSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 304
Db 249 SLSMTSAVQNSTYTTSVITSCSLTSSLSNLSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 308
Qy 305 APGTIMNGHGGGRSQOQLD 324
Db 309 APGTIMNGHGGGRSQOQLD 328

RESULT 6
US-10-176-758-252
; Sequence 252, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
```

us-10-509-307-1.1.rapb

Wed Feb 2 13:56:23 2005

125 SPFSQAKLRETPGSPSTVKNLLQLPSTTTIENISVSVHQPKHIKLAKRIPPASKIP 184
129 SPFSQAKLRETPGSPSTVKNLLQLPSTTTIENISVSVHQPKHIKLAKRIPPASKIP 188
185 ASAVEMPGSADVTGLNVQGALEFGSEPSLSFSGAPSENSNQIPISLYSKSISEPLNT 244
189 ASAVEMPGSADVTGLNVQGALEFGSEPSLSFSGAPSENSNQIPISLYSKSISEPLNT 248
245 SL5MTSAVQNSYTTTTSVITTSLSLTSLSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 304
249 SL5MTSAVQNSYTTTTSVITTSLSLTSLSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 308
305 APGTIMNHHGGGRSQOQLDT 324
309 APGTIMNHHGGGRSQOQLDLS 328
RESULT 6
US-10-174-581-252
Sequence 252, Application US/10174581
Publication No. US20030017540A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430RIC41
CURRENT APPLICATION NUMBER: US/10/174, 581
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063564
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063734
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063870
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066120
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066466
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066772
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069425
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: 60/069870
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/068017
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580

```
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086486
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087098
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087208
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088722
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: 60/089653
Query Match 37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 7 SSTAVNSCS--PQSLSSVLGSGFGLAPPKXANITSSQILDQLKAPSLGQTTTTPSTQON 64
Db 9 NSVLLRICSFIPLLKSSVLGSGFGLAPPKXANITSSQILDQLKAPSLGQTTTTPSTQON 68
Qy 65 STSHPTTTTSDLKPPPTSQSSVLSHLDFKSPSPVLSQLSQSQOQHQSOAVTTPPPGLE 124
Db 69 STSHPTTTTSDLKPPPTSQSSVLSHLDFKSPSPVLSQLSQSQOQHQSOAVTTPPPGLE 128
Qy 125 SFPSQAKLRESTPGDSPSTVKNLLQLPSTTTTENSVSVHQPPKHILAKRRIIPASKIP 184
Db 129 SFPSQAKLRESTPGDSPSTVKNLLQLPSTTTTENSVSVHQPPKHILAKRRIIPASKIP 188
Qy 185 ASAVEMPGSADVTGLNVQFGALEFGSPSESGFSGSPSSNSNQIPISLSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGALEFGSPSESGFSGSPSSNSNQIPISLSKSLSEPLNT 248
Qy 245 SLSMTSAVONSTYTTTSVITSCSLTSSSLNSASPVMSSSYDQSSVHNRIPIYQSPVSSSES 304
Db 249 SLSMTSAVONSTYTTTSVITSCSLTSSSLNSASPVMSSSYDQSSVHNRIPIYQSPVSSSES 308
Qy 305 APGTIMNGHGGRSQQTLD 324
Db 309 APGTIMNGHGGRSQQTLD 328

RESULT 7
US-10-176-483-252
; Sequence 252, Application US/10176483
; Publication No. US20030017541A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deenoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C68
; CURRENT APPLICATION NUMBER: US/10/176,483
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-483-252

Query Match 37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 7 SSTAVNSCS--PQSLSSVLGSGFGLAPPKXANITSSQILDQLKAPSLGQTTTTPSTQON 64
Db 9 NSVLLRICSFIPLLKSSVLGSGFGLAPPKXANITSSQILDQLKAPSLGQTTTTPSTQON 68
Qy 65 STSHPTTTTSDLKPPPTSQSSVLSHLDFKSPSPVLSQLSQSQOQHQSOAVTTPPPGLE 124
Db 69 STSHPTTTTSDLKPPPTSQSSVLSHLDFKSPSPVLSQLSQSQOQHQSOAVTTPPPGLE 128
Qy 125 SFPSQAKLRESTPGDSPSTVKNLLQLPSTTTTENSVSVHQPPKHILAKRRIIPASKIP 184
```

```
Db 129 SPFSQAKLRSTPGDPSFVNKLQLPSTTIENISVSHQPOPKHKLAKRIPPASKIP 188
QY 185 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSFSGAPSENSNQIPISLYSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSFSGAPSENSNQIPISLYSKSLSEPLNT 248
QY 245 SLMTSAVQNSTVTTSVITSCSLTSSLSNASPVAMSSSYDQSSVHNRIPIQSPVSSSES 304
Db 249 SLMTSAVQNSTVTTSVITSCSLTSSLSNASPVAMSSSYDQSSVHNRIPIQSPVSSSES 308
QY 305 APGTIMNHGGGRSQOQLDT 324
Db 309 APGTIMNHGGGRSQOQLDLS 328

RESULT 8
US-10-176-749-252
; Sequence 252, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C76
; CURRENT APPLICATION NUMBER: US/10/176,749
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-749-252

Query Match 37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 7 STAVNCS--PQSLSSVLGSGFGLAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 64
Db 9 NSVLLRIFCLPDKSSVLGSGFGLAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 68
QY 65 STSHPTTTTSDWKLPKPTSSQSVLHDLFKSQPEPSVLSQSRQHQSQAVTVPPGPLE 124
Db 69 STSHPTTTTSDWKLPKPTSSQSVLHDLFKSQPEPSVLSQSRQHQSQAVTVPPGPLE 128
QY 125 SPFSQAKLRSTPGDPSFVNKLQLPSTTIENISVSHQPOPKHKLAKRIPPASKIP 184
Db 129 SPFSQAKLRSTPGDPSFVNKLQLPSTTIENISVSHQPOPKHKLAKRIPPASKIP 188
QY 185 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSFSGAPSENSNQIPISLYSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSFSGAPSENSNQIPISLYSKSLSEPLNT 248
QY 245 SLMTSAVQNSTVTTSVITSCSLTSSLSNASPVAMSSSYDQSSVHNRIPIQSPVSSSES 304
Db 249 SLMTSAVQNSTVTTSVITSCSLTSSLSNASPVAMSSSYDQSSVHNRIPIQSPVSSSES 308
QY 305 APGTIMNHGGGRSQOQLDT 324
Db 309 APGTIMNHGGGRSQOQLDLS 328

RESULT 9
US-10-176-914-252
; Sequence 252, Application US/10176914
; Publication No. US20030017543A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C83
; CURRENT APPLICATION NUMBER: US/10/176,914
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-914-252

Query Match 37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 7 STAVNCS--PQSLSSVLGSGFGLAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 64
Db 9 NSVLLRIFCLPDKSSVLGSGFGLAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 68
QY 65 STSHPTTTTSDWKLPKPTSSQSVLHDLFKSQPEPSVLSQSRQHQSQAVTVPPGPLE 124
Db 69 STSHPTTTTSDWKLPKPTSSQSVLHDLFKSQPEPSVLSQSRQHQSQAVTVPPGPLE 128
QY 125 SPFSQAKLRSTPGDPSFVNKLQLPSTTIENISVSHQPOPKHKLAKRIPPASKIP 184
Db 129 SPFSQAKLRSTPGDPSFVNKLQLPSTTIENISVSHQPOPKHKLAKRIPPASKIP 188
QY 185 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSFSGAPSENSNQIPISLYSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSFSGAPSENSNQIPISLYSKSLSEPLNT 248
QY 245 SLMTSAVQNSTVTTSVITSCSLTSSLSNASPVAMSSSYDQSSVHNRIPIQSPVSSSES 304
Db 249 SLMTSAVQNSTVTTSVITSCSLTSSLSNASPVAMSSSYDQSSVHNRIPIQSPVSSSES 308
QY 305 APGTIMNHGGGRSQOQLDT 324
Db 309 APGTIMNHGGGRSQOQLDLS 328

RESULT 10
US-10-176-915-252
; Sequence 252, Application US/10176915
; Publication No. US20030017544A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
US-10-176-915-252
```

```
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C110
; CURRENT APPLICATION NUMBER: US/10/176,915
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-915-252

Query Match      37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 7 SSTAVNSCS--PQSLSSVLGSGFGLAPPKMANITSSQILDOLKAPSLGQFTTTPSTQON 64
Db 9 NSVLLRICSFIPLLKSSVLGSGFGLAPPKMANITSSQILDOLKAPSLGQFTTTPSTQON 68
Qy 65 STSHPTTTTSDWLKPPTSSQSVLSHLDFKSPSPVLSQSQHQHQSQAQVTPPPGLE 124
Db 69 STSHPTTTTSDWLKPPTSSQSVLSHLDFKSPSPVLSQSQHQHQSQAQVTPPPGLE 128
Qy 125 SFPQAKLRESTPGDSPSTVNKLQLPSTTIENISVSVHQPKHIKAKRRIIPASKIP 184
Db 129 SFPQAKLRESTPGDSPSTVNKLQLPSTTIENISVSVHQPKHIKAKRRIIPASKIP 188
Qy 185 ASAVEMPGSADVTGLNVQFGLERFSGPSLSEFGSAPSSSENSNOIPISLYSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLERFSGPSLSEFGSAPSSSENSNOIPISLYSKSLSEPLNT 248
Qy 245 SLSMTSAVONSTYTTSTVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 304
Db 249 SLSMTSAVONSTYTTSTVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 308
Qy 305 APGTIMNGHGGGRSQOQLDT 324
Db 309 APGTIMNGHGGGRSQOQLDLS 328

RESULT 11
US-10-173-706-252
; Sequence 252, Application US/10173706
; Publication No. US20030022293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C7
; CURRENT APPLICATION NUMBER: US/10/173,706
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-706-252

Query Match      37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 7 SSTAVNSCS--PQSLSSVLGSGFGLAPPKMANITSSQILDOLKAPSLGQFTTTPSTQON 64
Db 9 NSVLLRICSFIPLLKSSVLGSGFGLAPPKMANITSSQILDOLKAPSLGQFTTTPSTQON 68
Qy 65 STSHPTTTTSDWLKPPTSSQSVLSHLDFKSPSPVLSQSQHQHQSQAQVTPPPGLE 124
Db 69 STSHPTTTTSDWLKPPTSSQSVLSHLDFKSPSPVLSQSQHQHQSQAQVTPPPGLE 128
Qy 125 SFPQAKLRESTPGDSPSTVNKLQLPSTTIENISVSVHQPKHIKAKRRIIPASKIP 184
Db 129 SFPQAKLRESTPGDSPSTVNKLQLPSTTIENISVSVHQPKHIKAKRRIIPASKIP 188
Qy 185 ASAVEMPGSADVTGLNVQFGLERFSGPSLSEFGSAPSSSENSNOIPISLYSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLERFSGPSLSEFGSAPSSSENSNOIPISLYSKSLSEPLNT 248
Qy 245 SLSMTSAVONSTYTTSTVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 304
Db 249 SLSMTSAVONSTYTTSTVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 308
Qy 305 APGTIMNGHGGGRSQOQLDT 324
Db 309 APGTIMNGHGGGRSQOQLDLS 328

RESULT 12
US-10-175-738-252
; Sequence 252, Application US/10175738
; Publication No. US20030022294A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C45
; CURRENT APPLICATION NUMBER: US/10/175,738
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-738-252

Query Match      37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 7 SSTAVNSCS--PQSLSSVLGSGFGLAPPKMANITSSQILDOLKAPSLGQFTTTPSTQON 64
Db 9 NSVLLRICSFIPLLKSSVLGSGFGLAPPKMANITSSQILDOLKAPSLGQFTTTPSTQON 68
Qy 65 STSHPTTTTSDWLKPPTSSQSVLSHLDFKSPSPVLSQSQHQHQSQAQVTPPPGLE 124
Db 69 STSHPTTTTSDWLKPPTSSQSVLSHLDFKSPSPVLSQSQHQHQSQAQVTPPPGLE 128
Qy 125 SFPQAKLRESTPGDSPSTVNKLQLPSTTIENISVSVHQPKHIKAKRRIIPASKIP 184
Db 129 SFPQAKLRESTPGDSPSTVNKLQLPSTTIENISVSVHQPKHIKAKRRIIPASKIP 188
Qy 185 ASAVEMPGSADVTGLNVQFGLERFSGPSLSEFGSAPSSSENSNOIPISLYSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLERFSGPSLSEFGSAPSSSENSNOIPISLYSKSLSEPLNT 248
Qy 245 SLSMTSAVONSTYTTSTVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 304
Db 249 SLSMTSAVONSTYTTSTVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 308
Qy 305 APGTIMNGHGGGRSQOQLDT 324
Db 309 APGTIMNGHGGGRSQOQLDLS 328
```

US-10-176-482-252
; Sequence 252, Application US/10176482
; Publication No. US20030022296A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C70
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-482-252

Query Match 37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 7 SSTAVNSCS--PQSLSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQON 64
Db 9 NSVLLRICSFYLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQON 68
QY 65 STSHPTTTTSDWKLPPTQSQSVLHDLFKSQPEPSPVLSQLSQROHQSOAVTVPPPGLE 124
Db 69 STSHPTTTTSDWKLPPTQSQSVLHDLFKSQPEPSPVLSQLSQROHQSOAVTVPPPGLE 128
QY 125 SPFSQAKLRSTPGDSPSTVKNLQLPSTTTTENSVSVHQPPQPKHIKLAKRRIPPASKIP 184
Db 129 SPFSQAKLRSTPGDSPSTVKNLQLPSTTTTENSVSVHQPPQPKHIKLAKRRIPPASKIP 188
QY 185 ASAVEMPGSADVTGLNVQFGLFSGEPLSEFGAPSSSENSNQIPISLYSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLFSGEPLSEFGAPSSSENSNQIPISLYSKSLSEPLNT 248
QY 245 SLSMTSAVQNSTYTTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 304
Db 249 SLSMTSAVQNSTYTTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 308
QY 305 APGTIMNGHGGRSQOQLDT 324
Db 309 APGTIMNGHGGRSQOQLDLS 328

RESULT 15
US-10-176-752-252
; Sequence 252, Application US/10176752
; Publication No. US20030022297A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
US-10-176-752-252

Query Match 37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 7 SSTAVNSCS--PQSLSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQON 64
Db 9 NSVLLRICSFYLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQON 68
QY 65 STSHPTTTTSDWKLPPTQSQSVLHDLFKSQPEPSPVLSQLSQROHQSOAVTVPPPGLE 124
Db 69 STSHPTTTTSDWKLPPTQSQSVLHDLFKSQPEPSPVLSQLSQROHQSOAVTVPPPGLE 128
QY 125 SPFSQAKLRSTPGDSPSTVKNLQLPSTTTTENSVSVHQPPQPKHIKLAKRRIPPASKIP 184
Db 129 SPFSQAKLRSTPGDSPSTVKNLQLPSTTTTENSVSVHQPPQPKHIKLAKRRIPPASKIP 188
QY 185 ASAVEMPGSADVTGLNVQFGLFSGEPLSEFGAPSSSENSNQIPISLYSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLFSGEPLSEFGAPSSSENSNQIPISLYSKSLSEPLNT 248
QY 245 SLSMTSAVQNSTYTTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 304
Db 249 SLSMTSAVQNSTYTTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 308
QY 305 APGTIMNGHGGRSQOQLDT 324
Db 309 APGTIMNGHGGRSQOQLDLS 328

RESULT 14
US-10-175-752-252
; Sequence 252, Application US/10175752
; Publication No. US20030022295A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C60
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-752-252

Query Match 37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 7 SSTAVNSCS--PQSLSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQON 64
Db 9 NSVLLRICSFYLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQON 68
QY 65 STSHPTTTTSDWKLPPTQSQSVLHDLFKSQPEPSPVLSQLSQROHQSOAVTVPPPGLE 124
Db 69 STSHPTTTTSDWKLPPTQSQSVLHDLFKSQPEPSPVLSQLSQROHQSOAVTVPPPGLE 128
QY 125 SPFSQAKLRSTPGDSPSTVKNLQLPSTTTTENSVSVHQPPQPKHIKLAKRRIPPASKIP 184
Db 129 SPFSQAKLRSTPGDSPSTVKNLQLPSTTTTENSVSVHQPPQPKHIKLAKRRIPPASKIP 188
QY 185 ASAVEMPGSADVTGLNVQFGLFSGEPLSEFGAPSSSENSNQIPISLYSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLFSGEPLSEFGAPSSSENSNQIPISLYSKSLSEPLNT 248
QY 245 SLSMTSAVQNSTYTTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 304
Db 249 SLSMTSAVQNSTYTTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 308
QY 305 APGTIMNGHGGRSQOQLDT 324
Db 309 APGTIMNGHGGRSQOQLDLS 328

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC86
; CURRENT APPLICATION NUMBER: US/10/176,757
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-757-252

Query Match	37.9%;	Score 1536;	DB 14;	Length 363;
Best Local Similarity	96.2%;	Pred. No. 3.5e-79;		
Matches 308;	Conservative 3;	Mismatches 7;	Indels 2;	Gaps 1;

Qy	7	SSTAVNSCS--PQSLSSVLGSGFGLAPPKMANITSSQILDOLKAPSLGQFTTTPSTQON	64
Db	9	NSVLURICSFIPLLKSSVLGSGFGLAPPKMANITSSQILDOLKAPSLGQFTTTPSTQON	68
Qy	65	STSHPTTTTSDWKPTTSQSSVLSHLDPKSQPEPSVLSQLSQROHQHQSOAVTVPPGLE	124
Db	69	STSHPTTTTSDWKPTTSQSSVLSHLDPKSQPEPSVLSQLSQROHQHQSOAVTVPPGLE	128
Qy	125	SFPSQAKLRETPGDSPTVKNLQLPSTTTIENISVSVHQPOPKHIKAKRRIPPASKIP	184
Db	129	SFPSQAKLRETPGDSPTVKNLQLPSTTTIENISVSVHQPOPKHIKAKRRIPPASKIP	188
Qy	185	ASAVEMPGSADVTGLNVQFGLFSGEPSESLSEFGSAPSENSNQIPISLYSKSLSEPLNT	244
Db	189	ASAVEMPGSADVTGLNVQFGLFSGEPSESLSEFGSAPSENSNQIPISLYSKSLSEPLNT	248
Qy	245	SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPAMSSSYDOSSVHNRIPIQSPVSSSES	304
Db	249	SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPAMSSSYDOSSVHNRIPIQSPVSSSES	308
Qy	305	APGTMNGHGGGRSQQTLDLT	324
Db	309	APGTMNGHGGGRSQQTLDLS	328

Search completed: January 31, 2005, 17:49:12
Job time : 74 secs

This Page Blank (uspto)

Result No.	Score	Query Match	Length	DB	ID	Description
1	378.5	9.3	2232	2	T34434	hypothetical prote
2	360	8.9	1367	1	S48478	glucan 1,4-alpha-g
3	323	8.0	1802	2	S69703	HKRI protein precu
4	321	7.9	528	2	I47141	gastric mucin (Glo
5	314.5	7.8	1032	2	T34433	hypothetical prote
6	299.5	7.4	1104	2	S59310	probable membrane
7	291.5	7.2	534	2	T39903	serine-rich protei
8	289.5	7.1	1306	2	S25370	MSB2 protein - yea
9	286.5	7.1	2090	2	S26058	probable transform
10	280	6.9	2271	2	P90073	hypothetical prote
11	277	6.8	786	2	T15509	hypothetical prote
12	276.5	6.8	1630	2	A53577	ascites stialoglyco
13	274.5	6.8	1199	2	A0670	nuclear envelope p
14	274	6.8	1275	2	T33369	hypothetical prote
15	272.5	6.7	4776	2	E95206	cell wall surface
16	272	6.7	1063	2	D86731	hypothetical prote
17	270.5	6.7	2187	2	T30826	nascent polypeptid
18	270	6.7	3507	2	T34513	hypothetical prote
19	268.5	6.6	2715	2	T13049	eyelid - fruit fly
20	267	6.6	536	2	T37544	hypothetical serin
21	262.5	6.5	833	2	E90577	lipoprotein vsac [
22	261.5	6.4	583	2	S67571	hypothetical prote
23	260.5	6.4	1131	2	T41144	hypothetical serin
24	258.5	6.4	1804	2	H96597	hypothetical prote
25	257.5	6.4	1777	2	T34369	hypothetical prote
26	257.5	6.4	1952	2	T48814	hypothetical prote
27	254.5	6.3	3570	2	T45025	mucin MUC5B, trach
28	252.5	6.2	967	2	S66852	hypothetical prote
29	252	6.2	13288	2	T03099	mucin, submaxillar

Proc. Natl. Acad. Sci. U.S.A. 93, 8419-8424, 1996
A>Title: Muc1, a mucin-like protein that is regulated by Msi10, is critical for pseudohy
A;Reference number: JC6123; MUID:96323237; PMID:8710886
A;Accession: JC6123
A;Status: nucleic acid sequence not shown
A:Molecule type: DNA
A;Residues: 1-1367 <LAM>
A;Cross-references: GB:U30626; NID:gl1304386; PIDN:AAC49609.1; PID:gl1304387
C;Genetics:
A;Gene: SGD:MUC1; STA2; MAL5; DEK2; SGD:S0001458
A;Cross-references: MIPS:YIR019c; SGD:S0001458
A:Map position: 9R
C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase 1
C;Keywords: glycosidase; hydrolase; polysaccharide degradation; transmembrane protein
F:5-21/Domain: transmembrane #status predicted <TM1>
F:1350-1366/Domain: transmembrane #status predicted <TM2>

Query Match 8.9%; Score 360; DB 1; Length 1367;
Best Local Similarity 24.7%; Pred. No. 3e-09;
Matches 201; Conservative 103; Mismatches 328; Indels 182; Gaps 34;

QY 2 APTGSGTAVNSCSFQSLSSVLGSGFCELPKMANITSSQILDQLKAPSLGQFTTPT 61
Db 258 APATPTT---SCTKE-----KPTPTTCTCKE-----PTPHHDITPT 296
QY 62 QONSTSHPTTTTWDLPKPTSSQSVLGHDFKSOPEPSVLSLSQ-----RQHQSOA 115
Db 297 KKTTTCTCTKTTTPTPTSSST--TESSAPVPTPSSSTTESSAPVPTSTTSS 353
QY 116 VTPPPGLSPQAKURESTPGSPSTVNVKLLQLPSTTIENISVSHQPKHKLAKR 175
Db 354 APVPTPSSSTTES-----SSAPVTSSTTESAPVTSSTTESAPV--PTPSSSTTES 406
QY 176 RPPKAPKIPASAVEMPGSADVTGLNVQFALFEGSEP---SLSEFGSAP---SSENNOI 229
Db 407 SAPVTSSTTES-----SAPVTS-----STTESAPVTSSTTESAPVTSSTTES 456
QY 230 PISLYSKLSLSE---PLNTSLSMSTA--VQNSTVTTSTVITSCSLTSSLSNAS---PVAM 280
Db 457 PVPPTSSSTTESAPVTSSTTESAPVPTPSSSTTESAPVTSSTTESAPVPTPS 516
QY 281 SSSYQSSVHNRIPQSPVSS---SESAPGTIMHGCGGRSQQLTDTPKTTPPSALPSV 337
Db 517 SSTTESA-----PAPTSSSTTESAPV-----SSITESAPVPT-PSSTTES 564
QY 338 SSLPSTTCTCT---ALLPSTQHTGDLTSSPLSQLSSSHQSLSHAALSSSTSTH 393
Db 565 STPTVTSSTTESAPVPTPSSSTTESAPVPTPSS--TTESAPAPPTPSSSTTES 623
QY 394 ASVESASHQSGATFTSTAATSVSSASGVSLSGSMNTANSICLGTTPASASSSSRA-- 451
Db 624 APVTSSTTESAPVPTPSSSTTESAPVPTPSSSTTESAPVPTPSSSTTESAPV 683
QY 452 -----APLVTSKAPNLPQGVPPPLHNNQVILVPGGLPAYPIYGVDELMQLQSL 502
Db 684 TSSTTESAPVTSSTTESAPVPTPSSSTTESAPV--VPT-PSSTTESAPVPT 739
QY 503 PVDYIGIPFAAPTALASRRSLANNPDGVTKFGKDSASAPATTPAQ----- 552
Db 740 PSSSTTESAPVTSSTTESAPVPTPSSST-----TESAPVPTPSSSTTESAPV 794
QY 553 PQOSQQTHTTAQOPFVNALPGYGV-----TGLPYVTGMPSAFOGPTMFVPASA 605
Db 795 PTPSSSTTES-----VAPVPTPSSSNITSNAPSTPSSSTTESVVPVPTSSSTTES 849
QY 606 KQGVNLST-----PTP-----PFQASGVGHGYSYGYDGLTGATAA 643
Db 850 SSAPVSSSTTESVAPVPTPSSSNITSNAPSSITPSSST-----ESFST----- 894
QY 644 GDYSKGGYAGSQAQPNKSGSGPKGVSVSSSTTGLPDMTGSVYNTQTQFKGFHAGTP 703
Db 895 -----GTTVTPSSSKYPGSGQTSTSVSSSTTE-----TTIVPTKTTT-----SVTTP 934

QY 310 ---MNGHGGGRSQTLDLT---PKT-----TGPP--SAL 334
Db 1291 TGMWTHSGSTQTPSTIGSTVTPQSTVSGNSGSGTWTGSSSEASTSGSFKTSPSSISPV 1350
QY 335 PVSSSLPSTT-----SCTALLP-----STSQHTGLDT 361
Db 1351 PTSPPPTPTFASTSGSTISDVSVSTVTSAPLSSSLPSTVPSSSTQSPSTSESSSKAS 1410
QY 362 SSPL-SQLSSS---LSSHQSLSAHAALSSSTSHTHASVESASHQSGSATESTAA--SV 415
Db 1411 SSPVPSQSTSTPNTGSTEESTLLSSTISGSHQHTTMSKASGSGSTPSTNSQSTGVTM 1470
QY 416 SSASGSGVLSGSMNTANSICLGTTPASASSSSRAAPLVTSCKAPPNLPQGVPPLLHNO 475
Db 1471 GSSSTSGVSTSSAST-----QPMSTSQSSAGSTVASSTASPAASSTAPSSTGTM 1522
QY 476 YLVGPGGLPAYPIYGYDELMQLQSLRVDVYIGIPFAAPTALASRRSLANNPDGVTK 535
Db 1523 SSTSGTV-----GSTISESTTASASQSTGVTM 1553
QY 536 FGRGDSAPAPATPAQPOOSQ-----THHTAQOPFVNALPGYGVYTGLPYYTGMP 589
Db 1554 GSSSTSGVSTSSASTQPMSTSQSSAGSTVASSAGLVSTVTP--SSTGT---WGST 1608
QY 590 SAFQYGTPTFVPASAKQGVNLSTPTPPFQOASGVGHGYSYGYDDL--TQCTAAGD-- 645
Db 1609 SSGTVGSTITSESTTASAGSTGVTVMGSSSTSGVSTSSASTQPMSTSQSSAGSTV 1668
QY 646 -----YSKGVYAGSQAQPNKSA-----GSGPKGYS 671
Db 1669 ASSTTGLVSTVTPSTGTMGSSSTSGVSTGSTITSESTTASAGSTGVTVMGSSSTSGVS 1728
QY 672 VSSSTGLPDMTGSVYNTQTFDQGFHAGTPPPFSLPSVLGST--GPLASGAAP 724
Db 1729 TSSASSGQPMST-----QGSAGS-----TVVSTASPAASSTAP 1765

RESULT 2
S48478
glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae)
N:Alternate names: extracellular glucoamylase; mucin-like protein MUC1; protein YIR019c
C:Species: Saccharomyces cerevisiae
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S48478; B26877; S27281; JC6123
R:Rowley, K.
submitted to the EMBL Data Library, October 1994
A:Reference number: S48478
A:Accession: S48478
A:Molecule type: DNA
A;Residues: 1-1367 <ROW>
A;Cross-references: UNIPROT:P08640; GB:Z47047; EMBL:Z38061; NID:g603997; PID:g763364; GS
R;Yamashita, I.; Nakamura, M.; Fukui, S.
J. Bacteriol. 169, 2142-2149, 1987
A;Title: Gene fusion is a possible mechanism underlying the evolution of STAL.
A:Reference number: A91831; MUID:87194600; PMID:3106330
A:Accession: A26877
A:Molecule type: DNA
A;Residues: 1-242 <YAM>
A;Cross-references: EMBL:M16164; NID:g172522; PIDN:AAA35014.1; PID:g172525
A;Accession: B26877
A:Molecule type: DNA
A;Residues: 762-1331 <YA2>
A;Cross-references: EMBL:M16165; NID:g172523; PIDN:AAA35015.1; PID:g172526
R;Pardo, J.M.; Ianez, E.; Zalacain, M.; Claros, M.G.; Jimenez, A.
FEBS Lett. 239, 179-184, 1988
A;Title: Similar short elements in the 5' regions of the STA2 and SGA genes from Sacchar
A:Reference number: S27281; MUID:89031230; PMID:3141213
A:Accession: S27281
A:Molecule type: DNA
A;Residues: 1-31 <PAR>
A;Cross-references: EMBL:X13857; NID:g4551; PIDN:CAA32069.1; PID:g4552
R;Lambrechts, M.G.; Bauer, F.F.; Marmur, J.; Pretorius, I.S.

[illegible]

RESULT 4

```

I47141
gastric mucin (clone PGM-2A) - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I47141; S55315
R:Turner, B.S.; Bhaekar, K.R.; Hadzopoulou-Cladaras, M.; Specian, R.D.; LaMont, J.T.
Gastroenterology 106, 200, 1994
A:Title: Pig gastric mucin: isolation and characterization of a cDNA clone with a novel
A:Reference number: I47141; MUID:94102478; PMID:7506218
A:Accession: I47141
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-528 <TUR>
A:Cross-references: UNIPROT:Q29071; EMBL:U10281; NID:g915205; PIDN:AAC48526.1; PID:g915208
R:Turner, B.S.; Bhaekar, K.R.; Hadzopoulou-Cladaras, M.; Specian, R.D.; LaMont, J.T.
Biochem. J. 308, 89-96, 1995
A:Title: Isolation and characterization of cDNA clones encoding pig gastric mucin.
A:Reference number: S55315; MUID:95275264; PMID:7755593
A:Accession: S55315
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-528 <TUR>
A:Cross-references: GB:U10281; NID:g915205; PIDN:AAC48526.1; PID:g915208
C:Superfamily: pig submaxillary mucin

Query Match          7.9%; Score 321; DB 2; Length 528;
Best Local Similarity 23.2%; Pred. No. 6e-08;
Matches 181; Conservative 95; Mismatches 229; Indels 274; Gaps 28;

Qy  5  TGSSTAVNSCSPOSLSVLGSGFELAPPKMANITSSQILDQLKAPSLGFTTTPSTQON  64
Db  14  TTSTTSVQSSSSSV-----PIPTTSVQSSSSGSAFT----TSATSVQTS  55

Qy  65  STGHPTTTTSDWLKPTTSOSSVLSHLDFKSPQSPVLSQLSQROHQHQQAIVTPPPGLE  124
Db  56  SSSSSPPISTG--TSVOTSSSSS-----PTTSTTSVOPSSSSSAPTTRATSVQ  101

```

		Query Match	7.9%	Score 321;	DB 2;	Length 528;
		Best Local Similarity	23.2%;	Pred.No.6e-08;		
		Matches 181;	Conservative	95;	Mismatches 229;	Indels 274; Gaps 28
Qy	5	TGSGTAVNSCPQSLSVLGGFELAPPKXANTTSQILDQLKAPSLQGTTTTSTQQN	64			
		: : :	:	: : :	:	:
Dd	14	TTSTTSVQSSSSSV-----PIPSTTSVPSSSGAPT---TSATSVTQS	55			
Qy	65	STGHPTTTTWDLKPPTSQSSSVLSHLDKFQSQPEPSVLSQLSRQHQHQAATVVPPPGLE	124			
		: : :	:	: : :	:	:
Dd	56	SSSSEPPTSST--TSVOTSPSSSV-----PRTSTTSVOPSSSSSAPTTRATRSVO	101			

QY	125	SPPSQAKLRETPGSPSTVNNKLLQLPSTTIENISVSVHQPOPKHKLAKRRIPPAKIP	184
Db	102	SSSSSAPISSTVQPSSSG--SVPTTSATSVQSSSSSAP-----TTSATSVQ	150
QY	185	ASAVENPGADVTGLNVQGALEFGSEPSLSFEGAPSSSENQIPISLYKSLSEPLNT	244
Db	151	SSSSSPPISTVS-----VQPS--SSAPTTSATSVQ-----SSSSPPPISS	192
QY	245	SLSMTSAVONSTVTTSVITSSCLTSSLSNAGSPVAMSSSYDQSSVHNRIYQSPV--SSS	302
Db	193	TVSVQVQSSSSVPTTTSVQPSSSSVPTTSATSVRS--SSSSTPIPTTSVQPSSS	249
QY	303	ESAPGTIMNGHGGGRSQOQLDTPKTPGPSALPVSLSLSTCTALLPSTSQHGTDLTS	362
Db	250	SSAPTTSATSVQPSSSST-PIPSST--SVQPSSSSAPTTSATSVQPS--S	298
QY	363	SPLSQLSSLSHQSSLSAHAALSSSTSHASVESASHQSSATPSTAAATSVSSASG	422
Db	299	SP--PISSITSVQPSSS--SSPTTST-TSVQPSSSGAP--TTSATSVQPSSSS	347
QY	423	VSLSNMTANSICLGGTGPASASSSSRAAPLV---TSGKAPPNLPQGVPPPLHNOYLVG	479
Db	348	PISSISIV-----QPSSSSSPTTTSVQPSSSGAPTTSATSVQPSSS--	394
QY	480	PGGLLPAYPIGYDELMQSLRLPDYIYGIPFAAPTALASDRSLANNYPGDTVKEGRG	539
Db	395	-----SVPTTSATSVRS--S	409
QY	540	DSASPAPATTAPQOQSQTHTTAQPFVNPALPGYSYGLPYTGMPSAFQYGTMTF	599
Db	410	-SSTPIPTTSVQPSSSS	427
QY	600	VPPASAK--QGVNLSPTTFFQOAGYQGHGYSTGYNDLTQGTAAAGYKGYAGSSQA	657
Db	428	VPTTSATSVQTSSSSTPIPTTSVQ--	460
QY	658	PNKAGSGPGKGVSVSSSTGLPDMTGCVYKNTQTFDKQGFHAGTTPPFSLPSVLASTGP	717
Db	461	PTTSA-----TSVQPSSSSSPPISTI	486
QY	718	LASGAAPGYAPPPFLHLPAAHQPHSOLLHHLPQDAQSGGQSGORSPSSLPKQSKAPK	776
Db	487	SSSSSPTTTSV-----QPSSSGSAPTTSATSVQPSSSSPP	525
RESULT 5			
T34433			
hypothetical protein K06A9.1a - Caenorhabditis elegans			
C;Species: Caenorhabditis elegans			
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004			
C;Accession: T34433			
R;Geisel, C.; Gattung, S.			
submitted to the EMBL Data Library, December 1996			
A;Description: The sequence of C. elegans cosmid K06A9.			
A;Reference number: 221525			
A;Accession: T34433			
A;Status: preliminary; translated from GB/EMBL/DBJ			
A;Molecule type: DNA			
A;Residues: 1-1032 <GEI>			
A;Cross-references: UNIPROT:P91365; EMBL:U0846; PIDN:AAC70889.1; GSPDB:GN00028; CESP:K06A9			
A;Experimental source: strain Bristol N2; clone K06A9			
C;Genetics:			
A;Gene: CESP:K06A9.1a			
A;Map position: X			
A;Introns: 38/1; 75/3; 103/3; 132/2; 158/2; 222/1; 839/1; 849/1; 875/3; 940/2; 966/2; 99			
Query Match			
Best Local Similarity 7.8%; Score 314.5; DB 2; Length 1032;			
Matches 195; Conservative 98; Mismatches 284; Indels 199; Gaps 35;			
QY	5	TGSSTAVNSCSFQSL---SSVLGSGFGBELAPPKWANTTSQILDLQKAPSLGQTTTPTST	61

Db	224	TSPSTAVT--SPSLGTSSSPSPSSISSTALPIASSASS--SPSAAS--STTPV	273
QY	62	QONSTSHPTTTTNDLKPPTSSQSVLHLPKSPSPVLSQSRQHQOQVAVTVP	121
Db	274	LSSSTIOSSSGTF-----PSSVASSPSTVGTSGAASSSVATVSTTAGTGTIT-PVP	327
QY	122	GLESPFOAKLRETPGDSPTVNNKLLQLPSTTIENISVSVHQPOPKHKLAKRRIP--	179
Db	328	G-----SSSTIGSSTPSSASSSSSGTMTISGSGTSTTV-----VPGSS	366
QY	180	---ASKIPASAVEMPGSADVT---GLNVQFALFEGSEPSLSEFGSAPSSNSQ-----	228
Db	367	STFASSTPIASSSSPGST-VTVAPGSSSTYGS---STPSASSSSSGTMTNSGSGTGT	421
QY	229	--IPISLYSKLSLPLNTLSMTSAV-----QNSTYTTSVITSCSLTSSSLNSASPVAMS	281
Db	422	TVAPVSSSTFGSGSTPIASSSSSGTSTVVGSSSTYGS---TPSASSSSAGTASTISGS	478
QY	282	SSY-----DOSSVHNRIYQSPVSSSESAPGTIMNGHGGGRSQOQLDTPKTTGP-PSA	333
Db	479	TGSTATIVPGSSSSVGS---STQASAPSPSGTMTVSGTGTSTVTVVPGSSTSPAPSS	533
QY	334	LPSVSSLSSTCTALLPSTSQHGTDLTSPLSQLSSLSHQSSLSAHAALSSSTSTHTH	393
Db	534	SNPSSSPASTGTITISGSSIIIVSTVSG--STVSGTGTSTGLASTATPGSS--	588
QY	394	ASVESASSHQSSATPSTAAAT--SVSSASSSGVSLSSMNTANSICLGGTGPASASSSSRAA	452
Db	589	-TVPSSSPQPSQSPAPNTGTSTPSTQTSQSPSPSMNPSSS-----TPTGSSQT---	638
QY	453	PLVTSKAPPNLPQGVPPPLHNNQYLVPGLLPAYPIYGYDELMQSLRLPDYIYGIFPA	512
Db	639	--IT-----PEG-----STASSPTGSGTSTFS	658
QY	513	APTALASDRSLANNYPGDTVTKFGRDSASAPATTAPQOQSQSQTHHTAQPFVNPA	572
Db	659	VATEVTQ-----STVPSSSLGTQSTNSPSS--	688
QY	573	LPPGYSYTGLPYTGMPSAFQYGTMTFVPPASAKOHV--NLSTPTP-PFOAGSYGQHG	629
Db	689	LSP--STGMSLTISEPS-----PSSTQSSGAQSTLTTPSPNPQSSTSSLESST	735
QY	630	YSTGVDDLTOGTAAAGDYKGYAGSSQ---APNKASG--PGKGVSVSSST	676
Db	736	SGATTSSGAGTMTSPSSQSSVSGSTSPAASTTGEMTSGSTQSTPGSSVSTSAAI	795
QY	677	TGLPDMTGSVYKNTQTFDKQGFHAGTTPPFSLPSVLGSGTGPLASGA--APGYAPPP	730
Db	796	LTSQOQSVSTNPGSTVTRPSTVSGSTSGSTTVV-GSTEASTSGSLATTSAKP	850
RESULT 6			
S59310			
probable membrane protein YMR317w - yeast (Saccharomyces cerevisiae)			
N;Alternate names: hypothetical protein YMR924.09			
C;Species: Saccharomyces cerevisiae			
C;Date: 29-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 19-Apr-2002			
C;Accession: S59310			
R;Churcher, C.M.			
submitted to the EMBL Data Library, September 1995			
A;Reference number: S59302			
A;Accession: S59310			
A;Molecule type: DNA			
A;Residues: 1-1104 <CHU>			
A;Cross-references: EMBL:Z54141; GSPDB:GN00013; MIPS:YMR317w			
A;Experimental source: strain AB972			
C;Genetics:			
A;Gene: MIPS:YMR317w			
A;Cross-references: SGD:S0004936			
A;Map position: 13R			
Query Match			
Best Local Similarity 7.4%; Score 299.5; DB 2; Length 1104;			
Matches 22.8%; Pred. No. 1.4e-06;			

A:Map position: 7R
C:Superfamily: Yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase
C:Accession: S26058
C:Keywords: transmembrane protein
F:3-19/Domain: transmembrane #status predicted <TM1>
F:1189-1205/Domain: transmembrane #status predicted <TM2>

Query Match 7.1%; Score 289.5; DB 2; Length 1306;
Best Local Similarity 24.0%; Pred. No. 5e-06;
Matches 211; Conservative 110; Mismatches 365; Indels 193; Gaps 39;

QY 2 APTGSGTAVNSCPQSLGSGFGLAPKMANIT---SSQILDQ-----LKAPSL 52
DB 180 APLTSDTPLISTMAADNVFS-----ANPISALTTTDSSEFDQSTAGAPVQSS 234
QY 53 GQFTTT-----PSTQONSTSHPTTT--TSWDLKP-PTSQSS-----VLSHLDFKSQ 95
DB 235 ADSFSSSEILVQSADFSFSPSTTTDISLSAAPLOTSESSFTTASALPVSSTVDVGS 294
QY 96 PEPSVLSQLSQRCQHQSOQAVTVPPGLESFPQAKLRESTDSPSTVKNKLLQLP--ST 153
DB 295 -SASPVS-MSAAGQIASSSTDNPTMSETFSLTS--TEVDGSDVSTVSALLAPFLQT 350
QY 154 TIENISVHQPKHIKAKRIPPASKIPA-SAVEMPGSADVTGLNVQFGAL-----E 207
DB 351 STGN-SFSIVPS-----VSFVPSQSSDVASSSTANVVSSFSFDIPQGTST 396
QY 208 FGSEPSLSEFGSAPSSNSQIPISYKSLSEPLNTSLGMTSAVQNSTVTTVITSCSL 267
DB 397 SGSVVSVQAQASALAFQSTEV---YGASASSTMSSLLSTTS-LOSTLTDSSSLASSA 451
QY 268 TSSSL-----NSAPVAMSSYDQSSVHNRIPIQSPVSS-----SESAPTIMN 311
DB 452 SSSDLTDYGVSTASIPLLSASEQATSSSFVSFVSFVPSQSSDVAQSTAPVSS 511
QY 312 G-----HGGRSQQLDTPKTPPPALPSVSLPSTTCTALLPSTSGHGLTSSPL 365
DB 512 SFSYISLQAGSSMNPSSSTIVYSSSTGSEESAATAATLGGSSVTMAGNLQSQPP 571
QY 366 SOLSSSLSSHQSSLSAHAALSSSTSHT-----HASVE-----SASSHQSNATFS 409
DB 572 S--TSSLSEQATSTSAVLASSSVSTSPYTTAGGASTAEASSLSTSAETQVSVSQS 629
QY 410 TAATSVSSASSGV---SLSSSMTANSLCLGGTPASASSSSRAAPLVTSGKAPNLPQ 466
DB 630 TTAQTSSFASSTTEGETSSQGFSTSVLVQMPSSISSEFSPQTTQWNSASS-- 686
QY 467 GVPPLLHQYLVGPGLLP-----AYPIYGYDELMQSLRPVDYIGIPFAAPTALAS 519
DB 687 -----SQYTISSGTILLSQVSDTSVSYTTSSSSVQV--SDTPVSY-----TTSSS 729
QY 520 RDRSLANNPYGCVTKFGRGDSASAPATTPAQOQSQSQTHHTAQOQFVNPALPPGYSY 579
DB 730 SVSQVSDTP-----VSYTTSSSSVQVSDTPVSYTTSSSSVQVSDTP----- 772
QY 580 TCLPYVTGMPAFQYPTMFPVPSAKHQGVNLS--TPTPPPQAGSGYQCHGYSTGYDDL 638
DB 773 --VSYTTSSSSVQVSDTS--VPSISRSRSVQVSDTPVPSISRSVQ--TSSSLQPTT 827
QY 639 QCTAAGDYSKGGYAGSQAPNKSAGSGPKGVSVSSSTTGLPDMTGVSYNKTQTFDKQGF 698
DB 828 TSSQRTTISHGALSESSSVSQ-----SEITSSINATASEYHSIQ----- 870
QY 699 HAGTPTTSLPSVLGSGTGLASGAPGAPVPPFLHILPAHQPHSQLL-----HHHLPODA 754
DB 871 TAAATQ-----STTSLFTDANSSAS---APLEVATSTTPPSKASLLLTSTSSLSQVA 922
QY 755 QSGSGQRS-----OPSSILQPKSQASKPAYGNSPYW 784
DB 923 TTNVQTSLTSTTSTVLEPSTTNSSTTSLVTSDDNNW 961

probable transforming protein (can) - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S26058
C:Keywords: transmembrane protein
F:3-19/Domain: transmembrane #status predicted <TM1>
F:1189-1205/Domain: transmembrane #status predicted <TM2>

Query Match 7.1%; Score 286.5; DB 2; Length 2090;
Best Local Similarity 23.2%; Pred. No. 1.2e-05;
Matches 215; Conservative 104; Mismatches 349; Indels 257; Gaps 43;

QY 36 ANITSSQILDQKAPSLGQFTTTPSTQONSTSHPTTTTSMW-----LKPPTS 82
DB 965 ASLRSFSLSQRYVEDLDEVSTSVSQSLESEDARTCKDDEAVQAPRHAPVVRTPSI 1024
QY 83 QSSVL-----SHLDFKSP-----EPSPVLSQLSQRCQHQSOAVT--VPPGL 123
DB 1025 QPSLLPHAAPFAKSHLVHSGSPGVMTSVATSAKIIPOGADSTMLATKTVHGAPGESH 1084
QY 124 B-SFSPQ--AKLRESTDSPSTVKNKLLQLPSTTIENISVHQPOPKHIKAKRIPP 179
DB 1085 PISAPQQLAAALRQMASQAPA-VNTLTE---STLKNV-----PQVVNVQELKNP 1132
QY 180 A-----SKIPASAVEMPGS--ADVTGLNVQFGAL-----EPSEPSLSEFGSAPSSEN 225
DB 1133 ATPSTAMGSSVPYSTAKTPHPVLTPVAANQAKQSGLSINSLKPSGPTPASGQLSGDKASG 1192
QY 226 SNQIPISLYSK-----SLSEPLNTSLMTS---AVQNSTYTTVITSCSLSSSLNSASP 277
DB 1193 TAKITAVTSTPSAGQSKPFPSPSGTGNFNGIITTPPSNFTTAAQATPSTKESQ 1252
QY 278 VAMSSSYDQSSVHNRIPIQSPVSSSESAPGTIMNGHGGRSQQLDTPKTPPPALPSV 337
DB 1253 DAFSSGGGSKPYEALPSSSPSGITSAINT-----TPGEPA-----S 1291
QY 338 SSLPSTTCTALLPSTSGHGLTSSPLSQLSSLSHQSSLSAHAAL----- 385
DB 1292 SSRVPAPSGTAL--STTSKLETPPSKLGELFFPSLAGETLGSFSGLRVQADSTKPT 1349
QY 386 --SSSTS-----HTHASVESASSHQSSATFSTAATSVSS 417
DB 1350 NKASSTSLSTQPTKTSVPSGFNFTAPPVLGKHTEPPVTSSATTSVA--PPAATSTSS 1407
QY 418 SASSGVSLSSSMNTANSLCLGGTPASASSSSRAAPLVTSGKAPNLP---QGVPPLLHN 474
DB 1408 TAVFGSLPVTAGSSGVIISFGGTSLSAGKTSFSGSQQTNSTVTPSPAPPPTTAATPLPTS 1467
QY 475 QYLVGPGLL-----PAYPI-YGYDELMQSLRPVDYIGIPFAAPTALASRDRSLANNP 528
DB 1468 FPTLSFGSLSSATTPSLPMSAGRSTEEATSGALPKPGDSESVSAGSALLBEEQQQAQLP 1527
QY 529 YPGDVTKFGRGDSASAPATTPAQOQSQSQTHHTAQOQFVNPALPPGYSYTYGLPYTGM 588
DB 1528 QAPQOT-----SDSVKKEPVL--AQPAVNSGTAASSTSLV-----ALSABATPATTVG 1574
QY 589 PSFAFOYQPTMFPVPASA---KQHGYNL-----STPTP-----PQ 620
DB 1575 PDA---RTEAVPPASSFSFVGQTAVTAAAISSAGPVAIVETSTPTIASSTTIVAPGPSA 1630
QY 621 QASGYG-----QHGYSYTGVDLTCQTAAGDYSKG--GYAGSQAPNKSAGSG 665
DB 1631 EAAAFGTVTSSGVFAQPPAASSSSAFNQLNNTATAPATPVFGQVAASTAPS-LFGQQ 1689
QY 666 PGKGVSVSSSTTGLPDMTGVSYNKTQTFDKQGHAGTTPPPF--SLPSVLGST----- 715

Db 1690 TGSTASTAAT---PQVSSS-----GF---SSPAFGTTAPGVFGTTFQQAQSVF 1732
Qy 716 GPLASGAAP--GYAPPPPLHILPAHQPHSOLLHHHLFPQDAQSGS--CQRQPSLSLPKPS 771
Db 1733 GQSASSAASVFSQPGFSSV-PAFGPASS-----TPTTSGSVFGAASSTSSSSFS 1785
Qy 772 -----QASKPAYGNP 782
Db 1786 FQSSPNTGGGLFGQSNAPAFQSP 1810

RESULT 10
F90073
hypothetical protein SA2447 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: F90073
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:213111952; PMID:11418146
A:Accession: F90073
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2271 <KUR>
A:Cross-references: UNIPROT:Q990Y4; GB:BA000018; PID:g13702612; PIDN:BA843752.1; GSPDB:C
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA2447

Query Match 6.9%; Score 280; DB 2; Length 2271;
Best Local Similarity 22.3%; Pred. No. 2.6e-05;
Matches 166; Conservative 106; Mismatches 289; Indels 184; Gaps 23;

Qy 8 STAVNSCPQSLSSVLGSGE-LAPPKMANITQSILQDLKAPSLQOFTTTPSTQNST 66
Db 1088 STSGMSGASQDSMSISFSDSTSDSKSASTASGESISQASSTSGSVSTSLSTSN 1147
Qy 67 SHPTTTTSD-----LKPTQSSVLSHLDFKQPEPVLSQLSORQHOSQA 115
Db 1148 SERTSTSVSDSTSLSESISSTSDSISEA-ISAESTSISLSEGNSTSDSSQS 1206
Qy 116 VTVPPEGLSPQAKLRETPGSPSTVKNLQLPSTTIENISVHQPOPKHKLAKR 175
Db 1207 AS-----AFLSES-LSESTSESTSESV-----SSTSESTSL----- 1238
Qy 176 RIPPASKIPASAVEMPGSADVTGLNVQFALFEGFSPSLSEFGSAPSEN-SNOIPISL- 233
Db 1239 -----DSTSESGSTSLSGNSTSGSASIGSTSTISBSTSTFKSESVSTSLMST 1288
Qy 234 YKSLSLPLNTSL-MTSVAVONSTYTTVTITSCSLTSSLSNAS-PVAMSSYDQSSVHN 291
Db 1289 TSLNSTSLSTSLSDSTSDSKSLSTSMSTSDISSTKSDISSTSLSGSTSESE--- 1345
Qy 292 RIYQSPVSSSEAPGTMNGHGGGRSQOQLDTPKTPPALPSVSLPSTCTALLP 351
Db 1346 -----SDTSSSEK-----SDTSMISMSQSTSGSTST 1377
Qy 352 STQHTGDLTSSPLSLSSLSHQSLSAHAALSSSTSHTHASVSGASHQSGATFSTA 411
Db 1378 -STS-----LSDSTSLSLASMMQSGVDNSASQASNSTSTST-SESDSQSTSTVSQ 1431
Qy 412 ATSVSSSASSGVLSLSSMNTANSICLGG---TPASASSSSRAAPLVTSKAPNLPQGV 468
Db 1432 STQSESSTSTSLSDSTSLSTSKSTSQSGSTSTSLSGSESESDSISSTASESTESA 1491
Qy 469 PPLHNNQVLPVGGGLPAYPIYVDELQMLQSLRPVDYIGIPFAAPTALASRDRSLANNP 528
Db 1492 STLSLSDSTSTNSG-----SASTSTSLSNS- 1516
Qy 529 YPGDVTKFGRGDSASPAPA-TTPAQPOQSQTHTTAQQPFVNPALPPGYSTGLPYTGT 587

Db 1517 -----ASASESDSSTSLSDSTSGASMQSSESDSQSTSA----- 1549
Qy 588 MPSAFOYQPTMFVPPASAKQHGVNLSTPTTFFQAQSGVGHGYSTGVDDLTCGTAAAGDYS 647
Db 1550 -----SLSDLSLSTSTNMSTIASLSTSV-----STSESGSTSESTSDSTSLSDSQS 1600
Qy 648 KGYAGSSQAPNKSAGPGKGVSVSSSTTGLPDMTGVNVNKTQTFKQKQPHAGTTPPPFS 707
Db 1601 TSTRTSASGASSTSTSTSDSRSTASSTST-----MRTSTSDSQSNLSLSTSTST 1650
Qy 708 L-----PSVLGSGTGLGAAAPG 725
Db 1651 MSDSTSLSDSVSDSTSDSTASTSG 1675

RESULT 11
T16509
hypothetical protein F59A6.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16509
R;Nhan, M.
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of C. elegans cosmid F59A6.
A:Reference number: Z18526
A:Accession: T16509
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-786 <NHA>
A:Cross-references: UNIPROT:Q21027; EMBL:U41994; NID:g1123047; PID:g1123052; PIDN:AAA834
C:Genetics:
A:Gene: CESP:F59A6.3
A:Introns: 106/1; 620/1; 634/3; 675/3; 775/1

Query Match 6.8%; Score 277; DB 2; Length 786;
Best Local Similarity 22.1%; Pred. No. 1e-05;
Matches 174; Conservative 90; Mismatches 239; Indels 226; Gaps 29;

Qy 51 SLGQFTTTPSTQONS-----TSHPTTTTSDLKLPPTSQSVLSHL-----FKSQ-- 95
Db 17 ALSESSETPSTSLSCVWLGDSFATDKTNEYKGTCTSEAVBELESEMKWLKSEET 76
Qy 96 -----PEPSPVLSQSQORQHQSQAVTPPPGLESPFSAKLRETP 137
Db 77 TERNGLTQLFLCVKGACSDPSPWNTCTTSTASTFTI-----SSTSLKST- 126
Qy 138 GDSPTVKNLQLPSTTIENISVHQPOPKHKLAKRIPPASKIPASAVEMPGSADVT 197
Db 127 SDSTSTPRI-----STTDTKDTTTEDPVS---STDQSSTSPHETTRDTTTEGTTSEDT 179
Qy 198 GLNVQFALFEGSPS-LSEFGSAPSE-----NSNQIPISLYSKSLSEPL-----NT 244
Db 180 S-----TYGSTRSSRPKPTSEFTSTEDFTSTRSTSTSIETNSPSTVSTPEYDST 236
Qy 245 SLGMSAVQNSTYTTVSITS-----CSLTSSLSNASAPV-----A 279
Db 237 SSGNSETTESDGTITVFTTKDDTSTVSGDSNGSSTSEFKNTETTTGPGSTVSEPS 296
Qy 280 MSSSYDQSSVHN-----IPQSPVSSSES-----APGTMNGHGG-----RSQQT 321
Db 297 ERSDLSSSVSDRSTSDQDRTTBIGLQGPILSDSDNNPDPSTTSALTSGGTSTTSRASA 356
Qy 322 LDTPKTPGSPALPSVSLPSTTSCALLPSTQHTGLTSSP-----LSQLSSLSHQ 377
Db 357 SDPTTTPGTTSGSTASTTSGLSFSTSLGSSQSPGSSVTTTTPGSTTISGTSQTTSGPT 416
Qy 378 SLSAHAALSST-----SHTHASVESASSHQSSASTFSTAATSVSSSASGV 424
Db 417 TTSEPTTSGSTVSDTSGPSTTSGPSTTLGTSTTSGPSTTSGPSTTSGPSTTSGPSTTSGP 476
Qy 425 LSSSMNTANSLCIGGTPASASSSSSSRAAPLVTSKAPNLPQGVPLHNNQVLPVGGGL 484

Db

477 TSSGTV--STSGQSTSGTKTSTSGTSSG-----508

Qy

485 PAYPIGYDELOLQRLPVDYIGIPFAAPTALASDRSLANNP--YPGDVTKFGRGDSA 542

Db

509 -----PSTVSERTLSTSGPSTSGSTSTVST 539

Qy

543 SPAPATTPAQPOQ-----SQSQTHHTAQOFPFNPALPGYSVTGLPYITGMPSAFOYQPT 597

Db

540 TPCASITTSQSTSTSGPSTSGPSTASRSTVSTTSGP--STTSGPSTTSGPSTTS--GST 596

Qy

598 MFVPPASAKOHGYNLSTPTPPFQOAGYGHGYSTGYDDLTQCTAGDYSK--GGYAGSS 655

Db

597 KSTTSGPSTSGKNIST-----VSG-----KLTGTSISATISSAFGGNVFT 638

Qy

656 QAPNKAGSGPGKGVSVSSSTTGLPDMTGVVYKNTQTFKQGFHAGTTPPFLPSVLGST 715

Db

639 SKFSNSSGGTSSGKNFSQNTT-----SAANGTTQAVNNGSGSLPTNS-----SS 685

Qy

716 GPLASGAP 724

Db

686 GSSDSSTSP 694

RESULT 12

A53577

ascites sialoglycoprotein 1 - rat (fragments)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 07-Feb-1997

A;Accession: A53577

E;Wu, K.; Fregien, N.; Carraway, K.L.

J. Biol. Chem. 269, 11950-11955, 1994

A;Title: Molecular cloning and sequencing of the mucin subunit of a heterodimeric, bifur

A;Reference number: A53577; MUID:94216302; PMID:8163496

A;Accession: A53577

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1630 <WUA>

A;Cross-references: GB:U06746

C;Keywords: glycoprotein

Query Match 6.8%; Score 276.5; DB 2; Length 1630;

Best Local Similarity 20.9%; Pred. No. 2.6e-05;

Matches 205; Conservative 115; Mismatches 362; Indels 301; Gaps 40;

Qy

9 TAVNSCPQSLSVLGSGFGLAPPKMANITSSOILDLKAPSLGQTTTPSQONS--T 66

Db

133 TTTTSHAPRESS-----PP-----STSVIL-----TTTASTEGTSGDT 166

Qy

67 SHPTTTTSDWLKPTTSOSSVLSHLDFKSQPPSPV-----LSQLSORQHQSOAVT 117

Db

167 GHTNAVTTQGSTPATTEISVT-----PSTQKMSPVSTFSTSTQEIITLSQSHQTMKTT 221

Qy

118 VPPP-----GLSPFSQAKLRSTPGD-----SPSTVNKL-----QLPS 152

Db

222 RNPQTGTTEVTITLSASSSDHPSTSPSTPGTAPRTTSTTTTTLKVLMTLSLQQLP- 280

Qy

153 TTNIENISVHQ-----PPKHILAK-----174

Db

281 -TGSLGTSTQELTTLPSQSHQTMKTTSTRTQTTTPEVTRTTLSSASSDHQRETSSQT 339

Qy

175 -----RRIPPASKIPASAVEMPGSADVTGLNVQFALFPGSPSISEFGSA 220

Db

340 TLPSPDTTTSHPRESSPPSTSVILTHGREGTSGDTGHTM--AVTTQGSTPATTEISVT 397

Qy

221 PSENSNQIPISLYSKISEPLNTSLMTSAVQNSYTTTSTVITSCSLTSSSLNASPVAM 280

Db

398 PSTQKMS--PVSTFTSTQEIITLSQSHQTMKTRNPQRTTPEVTITLS-----448

Qy

281 SSSYDOSSVHNRIPYQSPVSSSESAPGTIMNGHGGRSQQTLDTPKT-----TGPPSAL 334

Db

449 ASSSDQVQVET-----TSRATLSFDTTTSHAPSVSSSPSTSTGTSVDGLITAV 501

Qy

335 PSVSLPST-----TSCTALLPSTSHQTDL---TSSP-----364

Db

502 TTQDSTPATTOGSLTSSQTLSTVSPPLSTGTQETSTQELTSSSQSHQTKMKTTHNPQTR 561

Qy

365 -----LSQLSSLSH-QSSLSAHLSSSTSHTHASVESASSHSSATFSTTAATSVSSA 419

Db

562 NTEVTITLSASSSDQVQVETTSQTLSDATTTSHAPRESSPPSTSDILITMASTEGTSG 621

Qy

420 SSGVSLASSMNTANSLCLGGTTPA---SASSSSRAAPLVTSKGAPNLPQGVPLLHNQ 475

Db

622 DTGHTMAVTTQ-----GSTPATTEISVTSTQKMSPVSTFTS---TQEIITLSQSQ 670

Qy

476 YLVGPGGLLPAY--PIYGYDELOLQRLPVDYIGIPFAAPTALASDRSLANNPYGDV 533

Db

671 H---TGGMKTTNRNQTGTEVTITLSASSSDQVQVETTSQTLSPDPTTTTSHAP-----722

Qy

534 TKFGRGDSASAPA---TTPAQPOQSOQTHHT-----AQQPFVNP 571

Db

723 ---RESSPPSTSDMLTTTASTEGTSGDTGHTTAVTTQGSIPATTTQTLSTTFASQKMTV 778

Qy

572 ALP-----PGVSYTG-----LPYYTGMPSAFOYQPTMFVP-----601

Db

779 STPTTSSIQELSTLPQSOHTGSMELSSRPQTTSVTLSLSSPSGSGTPTQTRSVTSSSDE 838

Qy

602 --PASAKOHGYNLSTP-----TPFQOAGYGHGYSTGYDDLTQGTAA-----GDYS 647

Db

839 TNPTSS---GVSNTSPATTEVLTPTSPSTPGTAPRTTETSTTTTKVLMTSLQKLP 895

Qy

648 KGYAGSSQAPNK-----SAGSGPGKGVSVSSSTTGLPDMTGVVYKNTQTFKQGFHAGT 702

Db

896 TGSTLTGS--TPTEVTITLSASSSDQVQVETTSQTLSPDATTSHAPRE-----SSS 946

Qy

703 PPFSL-----PSVLGSGTGLASGAAPGVAPPPP--LHILPAHQPHSLHHHLQD 753

Db

947 PFTSVILTMASTEGTSGDTGHTTAVTTQGSTPATTEISVTPTQKMTSTVLVTSTQE 1006

Qy

754 AOSGSGQSRQSPSSLPKQSKXP 776

Db

1007 LTSSQORTSGMGTSSKQPATTP 1029

RESULT 13

A40670

nuclear envelope protein POM 121 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

C;Accession: A40670

R;Hallberg, E.; Wozniak, R.W.; Blobel, G.

J. Cell Biol. 122, 513-521, 1993

A;Title: An integral membrane protein of the pore membrane domain of the nuclear envelope

A;Reference number: A40670; MUID:93328754; PMID:8335683

A;Accession: A40670

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1199 <HAL>

A;Cross-references: UNIPROT:P52591; GB:221513; NID:G396746; PIDN:CAA7925.1; PID:G396747

F;803-807,845-849,956-960,1010-1014,1047-1051,1076-1080/Region: pentapeptide motif (X-P-);

Query Match 6.8%; Score 274.5; DB 2; Length 1199;

Best Local Similarity 21.8%; Pred. No. 2.2e-05;

Matches 211; Conservative 113; Mismatches 336; Indels 309; Gaps 43;

Qy

7 SSTAVNSCPQSLSVLT-----GSGFGLAP-----32

Db

275 SSNAPDFCAKETVLNALKEKRTVAEBDLHLDOENKRRHDSGSGSHGSAPEPLVANG 334

Qy

33 -----PKMANI---TSSQILD-----OLKAPSLGQFTTT-----PSTQONSTSHPTTT 73

Db

335 VPAAFVPKPSLKRSLASQSSDHLNKRSTSSVSLTSTCTGIGIFSSRNAITSSVSST 394

Qy

74 S-----WDLKPTTSQSVSLHDLFKSQPSPVLSQLSORQHQH-----Q 114

Db

395 RGVSQLWKRGSTPS--SPFSSPASSRSGTTPERPAKKTREEPCHQSSSSAPLVTDKSSPGE 453

QY 115 AVTVPPGLESPFOAKLRES--TPCDSPSTVKNLQLPSTTIENISVSVHQPKHKL 172
Db KVTDPATG-----KQSLWTPPTPGSGQRKRKQLPLPSRRGDLTL-----PPPEL-- 502
QY 173 AKRRIIPASKIPASAVEMEGSADVTGLNVQFALFEGSEPSLSEFGSAPSENENQI--- 229
Db 503 -----GYSITAEEDLWERRASLQWFN---KVLK-----DKTODASTPATDTSPATSP 547
QY 230 -----PISLYSKLSRLPLNTSL-----SMTSAVQNSTVTS 260
Db 548 FTLTLPTVGPAAASPALPAPS-SNPLLLESKKMQESPAPSPSEPEEATVAAPSPKTPS 606
QY 261 VITCSLTSLSLNASPVAMSSSDQSVNHRIPYQSPVSSSESAPGTIMNGHGGRSQ 320
Db 607 LL--APLVSP---LTGPLASTSDSKPTT-----TFLGLASASSATPLTDTKAPGVSOAQL 657
QY 321 TLDTPKKTG-----PPSALPSVSLSPSTTSCTA-----LLPSTSOHTGDLTSS 363
Db 658 CVSTPAATAPSTPASTLFGMLSPASSSLATPGPACASPMFKPIFPATPKSESD---N 714
QY 364 PLSQLSSLSHSHQSLSAHAALSSSTGHT-----HASVESASSHOSSTAFSTAATSV-SSS 418
Db 715 PLPTSSAAATTPAS-TALPTTATATAHTPKPIFESVEPFAAMPPLSPFSLKQTATPAT 773
QY 419 ASSGVLSSSMNTANSCLGCTPASAS-----SSSRPAAPLVTS-----GKAPPN 463
Db 774 AATSAPLLTLGLTATSTVATGTTASAKPVFGFGVTTAASTASTIASTQSILFGGAPPV 833
QY 464 LPOGVPLLNHQLVPGCLLPAYPIYGYDELMQLSELVDYVYGIFFAAPTALASDRS 523
Db 834 TASSAPALASIFOGK-PLAPAAASVAGTSFSQ-----SLASSAQT 873
QY 524 LANNPYCDVTKFGRGDSAPAPATTPAQPOQSOT-HHTAQOPFVNPLPPGYSVTGL 582
Db 874 AASNSGSGFGGTLTSTISAPATT-SQPLTSTNTVTFNIPFASAKP-----AL 926
QY 583 PYYTGMSAFQYGTMFVPASAKQHGVNLSTPTPPFQOASGYQHGYSTGYDDLTOGTA 642
Db 927 PTYPGANSQPTFGAT-----DGATKPALAPSGSGSTFGNSVAS----- 965
QY 643 AGDYSGGYAGSQAOPNKSAGSGPKG---GVSVSSSTTGLPDMTGVSVYKNTQTFDKQ- 697
Db 966 -----APSAAPAPAFGGAAPAFGLKASASTFGFPASTQPAFGSTTSVFSFGS 1015
QY 698 -----FHAGTTPPFLPSVLGSTGPLASG-----AAGYAP 728
Db 1016 ATTSFGCAAAATTQTHSGSSSLFGSSTSPFTFG---GSAAPAGGGFGLSATPTGS 1072
QY 729 PPFLHILPAHQPHSOLLHHLPODAQSGS-----GORSQ-----KSQLP----- 772
Db 1073 T-----SGTFSFGSGSGTGTGTTTSFGGSLSQNTLGAPOQSFPFAPSVGSTP 1119
QY 773 ASKPAYGNS 781
Db 1120 ESKPVFGGT 1128

RESULT 14
T33369
hypothetical protein H02F09.3 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33369
R;Geisel, C.; Harmon, G.
submitted to the EMBL Data Library, July 1998
A;Description: The sequence of *C. elegans* cosmid H02F09.
A;Reference number: Z21330
A;Accession: T33369
A;Status: preliminary; translated from CB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1275 <GEI>
A;Cross-references: UNIPROT:O76602; EMBL:AF077538; PIDN:AAC64622.1; GSPDB:GN00028; CESP:
A;Experimental source: strain Bristol N2; clone H02F09

C;Genetics:

A;Gene: CESP:H02F09.3

A;Map position: X

A;Introns: 42/1; 78/3; 106/3; 135/2; 161/2; 224/1

C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase

Query Match 6.8%; Score 274; DB 2; Length 1275;

Best Local Similarity 22.2%; Pred. No. 2.5e-05;

Matches 170; Conservative 110; Mismatches 337; Indels 150; Gaps 26;

QY 4 GTGSGTAVNSCSQSLSSVLGSGFELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQQ 63
Db 427 GSGPSTAGTSLASTAVTTTSSGSSPTLPSPQSSTLSMSSLSTVTPSSSTAGATSPATQQ 486
QY 64 NSTSHPTTTTSDWLKPT-----SQSSVLSHLDKQPEPSPVL-----SQLSQRQHQ 112
Db 487 --STKPTIGTSMGPTTAVAGASTESTVLQ-----STPSGTTVTLPSGSGSTAGTSPQ 540
QY 113 SQAV-----TVPPPGLESFPQAKLRESTP---GDSPTVKNLQLPSTTIENISVSV 162
Db 541 ASTVTTVTDISTVSGSTVTSQTAESSLSTESPTSAAGSIISTVSVSQPSTYIP----- 594
QY 163 HQQPKHKLAKRIRIPASKI-----PASAVEMPGSADVTGLNVQFALFEGSEPS--- 213
Db 595 -----VSSASSIYTLGSGTGSTASPGTTESGSGSTSGPSTISGSSASTVT 640
QY 214 ---LSRFGSAPSSSENSNOIPISLYSKLSRLPLNTSLSMTSVAVQNSTVTSVITCSLTSS 270
Db 641 GSTVTEASTISGTESTSTIPGSTES-TVSEASTVSGSVSTVSGSTESTS---AGASTVSG 697
QY 271 SLMSASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAPGTIMNGHG-GRSQOQLDTPKTTG 329
Db 698 S--TGSTVSDSTISDSTGNTAPGSTESTVSGSVSTVSGSTGTPMTMSASTGSTNT 755
QY 330 PPALPSVSLPSTTCTALLPST-----SQHTG---DLTSSPLSLSSLSL---SHQS 377
Db 756 PGSTESTITDGTSTVSGSTGSGTGTNNPGSTDSSTTGISTVSGSLSTISGSGSTVSGSS 815
QY 378 SLNAAHALSSSTGHTHASVESASSHOSSTAFSTAATSVSSSSAGSGVLSMMNTANSCL 437
Db 816 DMTVSGTSSSGPSTESTVSGAST-MSPSTGSSVETISGSGSVSTVSGSTSSSTGSGSTV 874
QY 438 GGTVPASASSS---SRAAPLVTSKAPNLPQGVPPLLHNLQYLWPGGGLLPAYPIGYDE 494
Db 875 SSSSVTSVSESTISQSTGTTGES----- 900
QY 495 LQMLQRLPDYVYGIFFAAPTALASDRSLANNPYCDVTKFGRGDSAPAPATTPAQPO 554
Db 901 -----TVFGSGTATGSTMASASTGSDTTPGTESTITGTTV--GESTVSGSTG 949
QY 555 QSQSQTHHTAQOQFVNPPALPPGYSYTLGPYITGMPSAFOGPTMFVPPASAKQHGVNLST 614
Db 950 STITEGSTISEMTTMTVGVSTGTITGTESTVSGSTSTVTVGESTVSGSTEST 1009
QY 615 PTPPFOQASGYQHGYSTGYDDLTOGTAAGDYSGGYAGSGSQAPNKSAGSGPKGVSVSS 674
Db 1010 PTPV-STVSG-----STVGESTVSGSTASTSGSGSTSGSTAGSTVSGSS 1056
QY 675 STTGLPDMTGVSVYKNTQTFDKQFHAGTTPPFLPSVLGSGTGPLASG 721
Db 1057 AST-VTSSTGSGSTV-----SGS-----TVSTVSGSTGTITG 1092

RESULT 15

E95206

cell wall surface anchor family protein [imported] - *Streptococcus pneumoniae* (strain TI
C;Species: *Streptococcus pneumoniae*
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: E95206

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001

A:Accession:
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4776 <R>
A:Cross-references: UNIPROT:Q97P71; GB:AE005672; PIDN:AAK75846.1; PID:G14973269; GSPDB:G
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP1772

Query Match	6.7%	Score 272.5	DB 2	Length 4776
Best Local Similarity	20.1%	Pred. No. 0.00014		
Matches 146	Conservative 120	Mismatches 374	Indels 87	Gaps 8
QY	2	APGTGSGTAVNCSQPSQLSSVLGSGFCEGELAPPKMANITTSQILDQLKAPSLGQFTTTPST	61	
Db	2523	ASASASTSASBESASTSASASTSASASTSASASTSASASTSASVASTSASASTSASASTSAS	2582	
QY	62	QONSTSHPTTTTWDLKPPTSQSSVLSHLDFKSOPEPSPVLSQLSRQHQSOAVTVPPP	121	
Db	2583	ASTSASASTSASASASTSASASTSASASTSASASTSASASTSASASTSASASTSASASTS	2642	
QY	122	GLEFPQCAKURESTPGDPSPTVKNLLQLPPTTIENISVSHQPPQPKHKLAKERRIPPAS	181	
Db	2643	ASASASTSASASASTSASASASTSASASTSASASTSASASTSASASTSASASIASISAS	2702	
QY	182	KIPASAVEMPGSADVTGLNVQFALFEGSEPSLSEFGSAPSENSENQIPLISKSLSEUP	241	
Db	2703	ASASASTSASASTSASASTSASASTSASASIASISASASTSASASTSASASTSASASTS	2762	
QY	242	INTLSMTSAVO-NSTVYTTSVITSCGLTSSLSNLSASPVMSSSYDQSSVHNRIPIQSPVS	300	
Db	2763	ASTSASASTSASASASTSASASTSASASTSASASTSASASTSASASTSASASTSASAST	2816	
QY	301	SSESAPGIMNGHGGRSQQTLDPKTTGPPSALPSVSLPTTCTALLPSTSOHTGDL	360	
Db	2817	ASTSASASTSASASTSASASTSASASTSASASTSASVASTSASASTSASASTSASASTS	2876	
QY	361	TSSPLSQLSSLSHQSSLSAHAALSSSTSHTHASVESASHQSSASTFTTAATSVSSAS	420	
Db	2877	ASASTSASASTSASASTSASASTSASASTSASASTSASASTSASASTSASASTSASAST	2936	
QY	421	SGVLSSSMNTANSICLGGTPASASSSSSRAPLVTSCKAPPNLPGQVPLPHNQYLVP	480	
Db	2937	TSASEASTSASAS---ASTSASASTSASASTSASASTSASASTSASASTSASASTSAS	2974	
QY	481	GGLLPAYPIYDEQLQSLRVNDYVYGPFAAPTALASDRSLANNPYPGDVTKFGRGD	540	
Db	2975	-----ASTSASASTSASASTSASASTSASASTSASASTSASASTSASASTSASASTS	2992	
QY	541	SASAPATTPAQQOQSQTHHTAQOQFVNPALPGYVYTGLPYYTGMPSAFQYPTMFW	600	
Db	2993	TSASASTSASASTSASASTSASASTSASASTSASASTSASASTSASASTSASASTSAS	3049	
QY	601	PRASAKQHCNVNLSTPTPPQASGYGQHCYSGYDDLTQGGTAAGDYSKGGVAGSQAQNK	660	
Db	3050	-----SASE---SASTSTASASTSASESASTSASASTSASASTSASASTSASASTSAS	3103	
QY	661	SAGSGPGKGVSVSSSTTGLPDMTGVSYNKTQTFDKQGFHAGTTPPPPSLPVLGSTGPLAS	720	
Db	3104	SASESASTSASASTSASASTSASASTSASASTSASASTSASASTSASASTSASASTSAS	3156	
QY	721	GAAPGYA	727	
Db	3157	ASTSASA	3163	

Search completed: January 31, 2005, 17:47:30
Job time : 28 secs

Db	361	SHTHASVESAGSHQSSATFSTAATSVSSASGVSLSSSMMTANSLCLGGTPASASSSS	420					
Qy	450	RAAPLVTSGKAPNNLPQGVPPHLLHNOYLVGCGLLLPAYPIYGYDELMQLQSLPVDYGI	509					
Db	421	RAAPLVTSGKAPNNLPQGVPPHLLHNOYLVGCGLLLPAYPIYGYDELMQLQSLPVDYGI	480					
Qy	510	PFAAPALASRDRSLANNPYPGDVTKFGRGDSASAPATTTAAQPOQSOQTHHTAQQPFV	569					
Db	481	PFAAPALASRDRSLANNPYPGDVTKFGRGDSASAPATTTAAQPOQSOQTHHTAQQPFV	540					
Qy	570	NPALPPGYSYTGLPYITGMPSAFQVGTMPFVPPSAKOHGVLNSTPTPPFQOASGYGQHG	629					
Db	541	NPALPPGYSYTGLPYITGMPSAFQVGTMPFVPPSAKOHGVLNSTPTPPFQOASGYGQHG	600					
Qy	630	YSTGYDDLTCGTAAAGDYSXGGYAGSSQAQPKSAGSGPKGVSVSSTTGLPDMTGSVYNK	689					
Db	601	YSTGYDDLTCGTAAAGDYSXGGYAGSSQAQPKSAGSGPKGVSVSSTTGLPDMTGSVYNK	660					
Qy	690	TQTFDQKGFHAGTPPFSLPVLSGTGPIASNAQYAPPPFLHILPAHQOQHSOLLHHH	749					
Db	661	TQTFDQKGFHAGTPPFSLPVLSGTGPIASNAQYAPPPFLHILPAHQOQHSOLLHHH	720					
Qy	750	LPDAQSGSGORSQPSLQPKSQASKPAYGNSPYWTN	786					
Db	721	LPDAQSGSGORSQPSLQPKSQASKPAYGNSPYWTN	757					
RESULT 2								
Q812D6	PRELIMINARY; PRT; 1132 AA.							
ID	Q812D6							
AC	Q812D6;	2003 (TrEMBLrel. 24, Created)						
DT	01-JUN-2003	(TrEMBLrel. 24, Last sequence update)						
Dr	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)						
DE	Lingerer protein-1.							
GN	Name=Ubp2; Synonyms=lig-1;							
OS	Mus musculus (Mouse).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.							
OX	NCBI_TaxID=10090;							
RN	[1]							
RP	SEQUENCE FROM N.A.							
RX	MEDLINE=22412137; PubMed=12524348;							
RA	Kuniyoshi H., Baba K., Ueda R., Kondo S., Awano W., Juni N.,							
RA	Yamamoto D., a Drosophila gene involved in initiation and termination of							
RT	copulation, encodes a set of novel cytoplasmic proteins."							
RL	Genetics 162:1775-1789(2002).							
DR	EMBL; AF276965; AAO23024.1; -.							
DR	MGD; MGI:1916176; Ubp2.							
DR	InterPro; IPR000449; UBA.							
DR	InterPro; IPR009060; UBA_like.							
DR	Pfam; PF00627; UBA; 1.							
DR	SMART; SM00165; UBA; 1.							
SQ	SEQUENCE 1132 AA; 117935 MW; 48F091F992E3659A CRC64;							
Query Match								
Best Local Similarity 79.3%; Score 3214.5; DB 2; Length 1132;								
Matches 636; Conservative 46; Mismatches 98; Indels 25; Gaps								
Qy	1	MAPGTGSSAVNSCSPOSLSVLSGSGFELAPPKMANITSSQILDOLKAPSLGQFTTTPS	60					
Db	334	MAPGTANSTASASSYSPQSLVLSGSGFELPQSNMWNISNSQILDKLPGLSPFPASS	393					
Qy	61	TQONST-SHPTTTTMSDLKPPTSQSSVLSHLDFKSPQPSVLSQSQOQHSQAVTVP	119					
Db	394	AQONDASPPATTAANDLKPSAPQPSVLSRLDFKSPQPSVLSQSQOQHSQAVTVP	453					
Qy	120	PGLESFPQAKLRSTPGDSSTVKNKILQLPSTTIENISVSVHOPQPKHKLAKRRIPP	179					
Db	454	PGLESFSSLAKEPSTAGDPSTVSRLLQLPNMTVENI-VSAHQPOPKHKLPRRVPP	512					

RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	60
RA	Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,	61
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	62
RA	Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,	63
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	64
RA	Krzywinski M.I., Skalek U., Smallos D.B., Schnerch A., Schein J.E.,	65
RA	Jones S.J., Marra M.A.,	66
RT	"generation and initial analysis of more than 15,000 full-length human	67
RT	and mouse cDNA sequences";	68
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	69
RP	[2]	70
RP	SEQUENCE FROM N.A.	71
RC	STRAIN=Mix FVB/N;	72
RC	TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;	73
RC	Strausberg R.;	74
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.	75
RL	EMBL; BC007179; AA007179.1; -.	76
DR	MGD; MGI:1916176; Ubp2.	77
DR	InterPro; IPR000449; UBA.	78
DR	InterPro; IPR009060; UBA_like.	79
DR	Pfam; PF00627; UBA; 1.	80
DR	SMART; SM00165; UBA; 1.	81
SQL	SEQUENCE 1132 AA; 117965 MW; ECF8E72C9134BB38 CRC64;	82
Query Match	79.3%; Score 3214.5; DB 2; Length 1132;	83
Best Local Similarity	79.0%; Pred. No. 1e-124;	84
Matches	636; Conservative 46; Mismatches 98; Indels 25; Gaps 9;	85
QY	1 MAPGTGSGTAVNCSPOSLSVLGSGFGEIAPPKMANITSSQILDOLKAPSLGQFTTTPS	86
DB	334 MAPGTANSTGASSVSPSLSVLGGSGFGEIPOSNNVNINSQILDOLKAPSLGQFTTTPS	87
QY	61 TQGNST-SHEPTTTTSDWLKXPTTQSSVLSHLDFKSPVLSQSRQHQHQQAQVTP	88
DB	394 AQQNDTASPATTAANDLKFSAQPSVLSRLDFKSPVLSQSRQHQHQQAQVTP	89
QY	120 PPGLESPPSOAKLRESTPGDSPSTVNKLQLPSTTIENISVSVHQPOPKHKLAKRRIPP	90
DB	454 PPGLESFSSIAKPRESTAGDGPSTVSRLLQLPNNMTVENI-VSAHQPOPKHKLAKRRIPP	91
QY	180 ASKIPASAVEMPGSADVTGLNVQFGLFGESEPSLSFEGSAPS-SENSNQIPIISLYKSL	92
DB	513 ASKVPVSAVEMPGSSDVTGLNVQFGLFGESEPSLSFEGSAPS-SENSNQIPIISLYKSL	93
QY	239 SEPLNTSLMSTSAVQNSTYTTTSSVITSSCLSSSLNSASPVAMSSSYDQSSVHNRIPTQSP	94
DB	573 SEPLNASFPMTSAVQNSTYTTTSSVITSSCLSSSLNSASPVAMSSSYDQSSVHNRIPTQSP	95
QY	299 VSSSESAGPTIMNGHGGRSQOITLDT-----PKTTGPPSALPSVSLPSTTSCALLPS	96
DB	633 ASPDPSAGPSVANGHGGRSQHTVDTTSSVPAPKKT-DPSALPSVSLPSPASCTALLPS	97
QY	353 TSQHT-----GDLTSSPLSOLSSLSHQSSL-SAHAAALSSSTSHTHASVEASS	98
DB	692 SAQHTATLPSTPAAEELSSPLSQSSSLSGHNSMTSAHATRSTSTPHTHASVESTA-	99
QY	402 HQSSATPSTAAATSVSSASGVSLSSSMTANSICLGCTPASASSSSRAAPLVTSCAP	100
DB	751 --SSAAFAAATSAAPSAGSVGLPGSMSTVSSLCIGTTVSVSPSSSTRATALTSCAP	101
QY	462 PNLPGQVPPLLHNOYLVGPGLLPAYPIYGYDELOMLQSLRPVDYIGYIPFAAPTALASRD	102
DB	809 PNLPGQVPPLLHNOYLVGPGLLPAYPIYGYDELOMLQSLRPMDYIGYIPFAAPTALASRD	103
QY	522 RSLANNPYCDVTKFGRGDSASAPATTPAQPOQSQTHTTAQOQFPFNALPGYSYTG	104
DB	869 GNLANNPYGDVTKFGRGDSASAPATTPAQPOQSQTHTTAQOQFPFNALPGYSYTG	105
QY	582 LPYITGWPSAFYQPTMTFVPPSAKOHGVNLSTPTTTPFQOASGYGQHGYSTGYDDLQGT	106
DB	929 LPYITGWPSAFYQPTMTFVPPSAKOHGVNLSTPTTTPFQOASGYGQHGYSTGYDDLQGT	107
QY	642 AAGDYSGGYAGSSQAPNKASGPGKGVSVSSSTGLPDMTGSVYNKTTQTFQKQGFHAG	108

Db	989	AAGDYTKGGYGGSSQAPNKSITGSGPGKGVSVSSG-TCLPDMTGSVNVNKTTQTFDKQGFHAG	1047		
Qy	702	TPPFSLPSVLGSTGPLASGAAPGYAPPFLHTLPAHQPHSOLLHHLLPODAOSGSGQR	761		
Db	1048	TPPFSLPSALGSTGPLAAPAAAPGYAPAFPLHMPAQPHSQULLHHLLQQDAPSQGQR	1107		
Qy	762	SQPSSLQPKSQASKPAYGNSPYWTN	786		
Db	1108	SQPSSLQPKSQASKPTYGSAPYWTN	1132		
<hr/>					
RESULT 4					
ID	QBNC94				
ID	AC	PRELIMINARY;	PRT; 597 AA.		
DT	01-OCT-2002	(T-EMBLrel. 22, Created)			
DT	01-OCT-2002	(T-EMBLrel. 22, Last sequence update)			
DT	01-MAR-2003	(T-EMBLrel. 23, Last annotation update)			
DE	Hypothetical protein FLJ90403.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Isoqai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,				
RA	Suzuki Y., Nagai K., Sugano S., Ichii S., Kawai-Hio Y., Saito K.,				
RA	Yamanoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,				
RA	Masuno Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,				
RL	Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;				
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AK074884; BAC11266.1; --				
DR	GeneW; HGNC:14185; URAP2.				
SQ	SEQUENCE 597 AA; 60780 MW; DBD70598D935F1E CRC64;				
<hr/>					
Query Match 76.0%; Score 3083; DB 2; Length 597;					
Best Local Similarity 99.7%; Pred. No. 1.4e-119;					
Matches 595; Conservative 1; Mismatches 1; Indels 0; Gaps 0;					
<hr/>					
Qy	190	MFQSADVTGLNVQFGALEFGSEFPISLSEFGSAPSSSENSNQIPISLSYSKLSLEPLNTSLSWT	249		
Db	1	MFQSADVTGLNVQFGALEFGSEFPISLSEFGSAPSSSENSNQIPISLSYSKLSLEPLNTSLSWT	60		
<hr/>					
Qy	250	SAVQNSTYTTSVITSCSLTSSLSNASPVAMSSSYDQSSVHNRIPIQSPVSSSESAPGTI	309		
Db	61	SAVQNSTYTTSVITSCSLTSSLSNASPVAMSSSYDQSSVHNRIPIQSPVSSSESAPGTI	120		
<hr/>					
Qy	310	MNGHGGRSQOQLDTPKTTPGPSALPSVSSLPSTTCTALLPSTSOHTGDLTSSPLSQLS	369		
Db	121	MNGHGGRSQOQLDTPKTTPGPSALPSVSSLPSTTCTALLPSTSOHTGDLTSSPLSQLS	180		
<hr/>					
Qy	370	SSLSSHQSLSAHAALSSTSTHSHAVESASHQSATSFTATSVSSSASSGVSLSSSM	429		
Db	181	SSLSSHQSLSAHAALSSTSTHSHAVESASHQSATSFTATSVSSSASSGVSLSSSM	240		
<hr/>					
Qy	430	NTANSLICLGTPPASASSSSSRRAPIVTSKCAPNLPGVPPLLHQYLPGCGLLPAYPI	489		
Db	241	NTANSLICLGTPPASASSSSSRRAPIVTSKCAPNLPGVPPLLHQYLPGCGLLPAYPI	300		
<hr/>					
Qy	490	YGVDLQMLQSLRPVDYTGIFPAAPTALASRDRLANNYPGDVTKFGRGDSASPAPATT	549		
Db	301	YGVDLQMLQSLRPVDYTGIFPAAPTALASRDRLANNYPGDVTKFGRGDSASPAPATT	360		
<hr/>					
Qy	550	PAQPOQSQSTHTTAQPPVNPALPPGVSYTGLPYITGMPSAFQVPTWFVPASAKQH	609		
Db	361	PAQPOQSQSTHTTAQPPVNPALPPGVSYTGLPYITGMPSAFQVPTWFVPASAKQH	420		
<hr/>					
Qy	610	VNLSTPTPPFOAQSGVGHGYSTGYDDLTQTGAAGDYSKGKYAGSSQAOPNKAGSGPGK	669		
Db	421	VNLSTPTPPFOAQSGVGHGYSTGYDDLTQTGAAGDYSKGKYAGSSQAOPNKAGSGPGK	480		
<hr/>					
Qy	670	VSVSSSTTCGLPWMTGSVNVNKTTQTFDKQGFHAGTPPPFSLPSVLGSGTPLASGAAPGYAPP	729		

Db	481	VSVSSSTTGLPDMTGSVYNTQTFDKQGFHAGTTPFPFSLPSVLGSLGASGAAPGYAPP	540
Qy	730	PFLHILPAHQPHSOLLHHLHPDQAQSGSGQSQSSLOPKSQASKPAYGNSPYWTN	786
Db	541	PFLHILPAHQPHSOLLHHLHPDQAQSGSGQSQSSLOPKSQASKPAYGNSPYWTN	597
RESULT 5			
Q99K40		PRELIMINARY; PRT; 700 AA.	
AC	Q99K40		
DT	01-JUN-2001	(T-EMBLrel. 17, Created)	
DT	01-JUN-2001	(T-EMBLrel. 17, Last sequence update)	
DT	01-OCT-2003	(T-EMBLrel. 25, Last annotation update)	
DE	Ubp2 protein (fragment)		
GN	Names=Ubp2;		
OS	Mus musculus (Mouse)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=mix FVB/N;		
RC	TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;		
RX	MEDLINE=22388257; PubMed=1247932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RP	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=mix FVB/N;		
RC	TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;		
RA	Strausberg R.;		
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC005482; AA05482.1; --		
DR	MGD; MGI:1916176; Ubp2.		
FT	NON_TER		
SQ	SEQUENCE 700 AA; 71456 MW; DD2C8296DCASF8ED CRC64;		
Query Match	71.6%; Score 2902; DB 2; Length 700;		
Best Local Similarity	80.9%; Pred. No. 4.7e-112;		
Matches	571; Conservative 39; Mismatches 72; Indels 24; Gaps 8;		
Qy	99	SPVLSOLSOQHOQSOAVTPPPGLSPPOAKLRESTPGDSPSTVKNKLLQLPSTTIENI	158
Db	1	SPVLSOLSOQHOQSOAVTPPPGLSPPOAKLRESTPGDSPSTVKNKLLQLPSTTIENI	60
Qy	159	SVSVHQPQPKHKLAKRRIPPAKIPASAVEMPGSDVTGLNVQFALFQSGPSLSFEG	218
Db	61	-VSAHQPPQKHKLKRRIPPAKIPASAVEMPGSDVTGLNVQFALFQSGPSLSFEG	119
Qy	219	SAPG-SENENQIPISLYKSLSEPLNTSLMTSAVQNSYTTTSLVITSCSLTSSLSNLSASP	277
Db	120	SAASASENSNQIPISLYKSLSEPLNTSLMTSAVQNSYTTTSLVITSCSLTSSLSNLSASP	179
Qy	278	VAMSSSDOSSVHNRIPIYQSPVSSSSAPCTIMNGHGGGRSQOTLDT-----PKTGTGP	331
Db	180	VTTSSSDOSSVHNRIPIYQSPVSSSSAPCTIMNGHGGGRSQOTLDT-----PKTGTGP	238
Qy	332	SALPVSLSLSTTCTALLPSTSQHT-----GDLTSSPLSOLSSLSHSSSL-S	380
Db	239	SALPVSLSLSTTCTALLPSTSQHT-----GDLTSSPLSOLSSLSHSSSL-S	298
Qy	381	AHAALSSSTSHTHASVESASSHSSATFTAAATSVSSASSGVSLSMNTANSLCLGGT	440
Db	299	AHAATRSTSTPHTHASVESTA---SSAFAAAATSAFAPSSGVLPGSMSTVSSLCGGT	355
Qy	441	PASASSSSRAAPLVTSCKAPPNLPQGVPPLLHNQYLVGPGGLPAYPIYGYDELOMLQS	500
Db	356	TVSPSSSTRATALTSGKAPPNLPQGVPPLLHNQYLVGPGGLPAYPIYGYDELOMLQS	415
Qy	501	RLPVDYIGIPFAAPTALASDRSLANNPYEGDVTKFGSGDSASAPATTPAQOQSQT	560
Db	416	RLPMDYIGIPFAAPTALASDRSLANNPYEGDVTKFGSGDSASAPATTPAQOQSQT	475
Qy	561	HHTAQOQFVNAPLPPGYSYTGLPYTGTMPSAFOVGTMPFVPPASAKQGVNLSSTPTPPFQ	620
Db	476	HHTAQOQFVNAPLPPGYSYTGLPYTGTMPSAFOVGTMPFVPPASAKQGVNLSSTPTPPFQ	535
Qy	621	QASGYGQHGYSTGYDDLTQGTAAADYSGKGYAGSQAPNKSAGSGPKGYSVSSSTGLP	680
Db	536	QASGYGQHGYSTGYDDLTQGTAAADYSGKGYAGSQAPNKSAGSGPKGYSVSSSTGLP	594
Qy	681	DMTGSVYNTQTFDKQGFHAGTTPFPFSLPSVLGSLGASGAAPGYAPPFHLHPAHQ	740
Db	595	DMTGSVYNTQTFDKQGFHAGTTPFPFSLPSVLGSLGASGAAPGYAPPFHLHPAHQ	654
Qy	741	PHSOLLHHLHPDQAQSGSGQSQSSLOPKSQASKPAYGNSPYWTN	786
Db	655	PHSOLLHHLHPDQAQSGSGQSQSSLOPKSQASKPAYGNSPYWTN	700
RESULT 6			
Q9POH6		PRELIMINARY; PRT; 583 AA.	
AC	Q9POH6		
DT	01-OCT-2000	(T-EMBLrel. 15, Created)	
DT	01-OCT-2000	(T-EMBLrel. 15, Last sequence update)	
DT	01-MAR-2004	(T-EMBLrel. 26, Last annotation update)	
DE	AD-012 protein.		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Adrenal gland;		
RA	Gu Y., Fu S., Ren S., Jin W., Gu J., Huang Q., Dong H., Yu Y., Fu G.,		
RA	Wang Y., Chen Z., Han Z.;		
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF157327; AAF67493.1; --		
DR	InterPro; IPR000449; UBA.		
DR	InterPro; IPR000449; UBA.		
DR	Pfam; PF00627; UBA; 1.		
DR	SMART; SM00165; UBA; 1.		
SQ	SEQUENCE 583 AA; 60706 MW; 65B0F16F16658FA6 CRC64;		
Query Match	43.1%; Score 1746.5; DB 2; Length 583;		
Best Local Similarity	81.2%; Pred. No. 1.6e-64;		
Matches	345; Conservative 16; Mismatches 45; Indels 19; Gaps 6;		
Qy	359	DLTSSPLSOLSSLSHSSATFTAAATSVSSASSGVSLSMNTANSLCLGGT	417
Db	128	ELSSSPLSOLSSLSHSSATFTAAATSVSSASSGVSLSMNTANSLCLGGT	184
Qy	418	SASGVSLSMNTANSLCLGGTTPASASSSSPAAPLVTSCKAPPNLPQGVPPLLHNQYL	477
Db	185	APSSGVSLSMNTANSLCLGGTTPASASSSSPAAPLVTSCKAPPNLPQGVPPLLHNQYL	244

Qy 478 VPGGLLPAYPIYGYDELOMLQSLRPVYDYGIPFAAPTALASDRSLANNPYDGDVTKFG 537
Db 245 VPGGLLPAYPIYGYDELOMLQSLRPVYDYGIPFAAPTALASDRSLANNPYDGDVTKFG 304
Qy 538 RGDASAPATTP-----AQPOOSQTHHTAQQFV--NPALPGYSGVTGLPYTGMPSA 591
Db 305 RGDASAPATTP-----TAHSPAALRESCTATWYSYTGIPYTGMPSA 358
Qy 592 FOYGTWFPVPASAKQHGWNLSSTPPFQOASGYGQHGYSYDGLDQTGTAAGDYSKGY 651
Db 359 FOYGTWFPVPASAKHGWNLSSTPPFQOASGYGQHGYSYDGLDQTGTAAGDYSKGY 418
Qy 652 AGSSQAPNKSAGSGPGKGVSVSSSTGLPDWMTGVSYNKTKTQDQGFAGTTPPFLPSV 711
Db 419 AGSSQAPNKSAGSGPGKGVSVSSSTGLPDWMTGVSYNKTKTQDQGFAGTTPPFLPSV 478
Qy 712 LGSTGPLASGAAGYAPPPFLHILPAHQPHSLHLLHLLPQDAGSGSGQSRSPSLQPKS 771
Db 479 LGSTGPLAQAAGYAPPPFLHILPAHQPHSLHLLHLLPQDAGSGSGQSRSPA---PCS 535
Qy 772 QASKP 776
Db 536 PSLKP 540

RESULT 7

ID Q9BTU3 PRELIMINARY; PRT; 1087 AA.
AC Q9BTU3, 2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE NICE-4 protein.
EN Name=NICE-4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strauberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC003170; AA003170.1; -
DR InterPro: IPR000449; UBA.
DR InterPro: IPR009060; UBA_like.
DR Pfam: PF00627; UBA; 1.
DR SMART: SM00165; UBA; 1.

DR PROSITE; PS00030; UBA; 1.
SQ SEQUENCE 1087 AA; 114543 MW; 038995DCCD570C2F9 CRC64;
Query Match 39.4%; Score 1599; DB 2; Length 1087;
Best Local Similarity 46.2%; Pred. No. 3.6e-508; Indels 130; Gaps 33;
Matches 386; Conservative 111; Mismatches 208;
Qy 3 PGTGSSAVNASCPSQSLSSVLGSGFELAPPKMANITSSQILDQLK-APSLGQTTTPTST 61
Db 327 PASG-----NTFHHHSMVSMGLKGFVDGVEAKGSGTTGSGFLEQFKTAQALAA---- 377
Qy 62 QQNSTSHPTTTTSDWLKPPTSQSSVLSHLDFKSOPEPSPVLSQSRQ----- 109
Db 378 -QHSQSGSTTTSSNDM-GSTTQSPSLVQYDLKN-PSDSAVHSPFTKQAFTPSSMEVF 434
Qy 110 -QHSQAV---TVPPPGLESFSPQAKLRESTDGSPSTVYKLLQLSTTIENTISVSHQ 164
Db 435 LQKSPAVATSTAAPPPSPPLFSK---TSAPQMSFG-----SSDNQSSS--- 477
Qy 165 PQQPHIKL--AKRRIPPASIPASAVEMPGSADVTGLNVQFALFEGSEPSLSFSGAP- 221
Db 478 PQAQKQLKQKKKASLTSKI PALAVEMPGSADISGLNLQFALQFGSEPVLSYESTPT 537
Qy 222 SSNSNQIPISLYSKSLSEPLNTSLMSTAVQNSYTTTTSVITSCSLTSSSLNSLSPVMS 281
Db 538 TSASSSQAPSSLYTSTASESSSTISSNQ--QESGYQSGPIQSTTYSQN-NAQGPL--- 591
Qy 282 SSYDQSSVHNRIYQSPVSSSESAPGT-IMNHGCGRSQQLDTPKTTGP-----PSALP 335
Db 592 --YEORSTQTR-RYPSSISSPQKDLQAKNGFSSVQATQLQTQSVVEGATGSAVKDSP 648
Qy 336 SVSSSLP---STTCTALLPSTSQHTG-----DLTSPLSQLSSLSHSHQSLSAHA 383
Db 649 STSIPPLNETVSAASLLTTNQHSSSLGSLHSEIEPTNTTQHSSTLSLQQTWLSST 708
Qy 384 ALSSTSTHT--HASVES-ASSHOSSTATFTAAATSVSSASGVSLSLSSMTANSLCLGTT 440
Db 709 SSGRTSTTLHTSVSEANLHSSSTFTSTSTSVSAPPV-VSVSSSLNSGSSLSGLSLG 767
Qy 441 PASASSSSRAAPLVTSGKAPNLPQGVPPHLLNQYLVGPGLLPAYP--IYGYDELOML 498
Db 768 SNSTVTASTRSSVATTSGKAPNLPQGVPPHLLNPYIMAP-GLLHAYPPQYGYDDLOML 826
Qy 499 QSLRPVDYDYGIPFAAPTA-LASDRSLANNPYDGDVTKFGSGSASAPATTPAQPOSQ 557
Db 827 QTTFPLDYISIPFTPTPLTGDSLASNPIYSGDLTKFGRGDASSAPATTLAQPONQ 886
Qy 558 SQTHHTAQQFVNPALPPGYSTGLPYT---GMPSAFQYGTMF-VPPASAKQHGWNLS 613
Db 887 TQTHHTTQQTFLNPAFPYGYSTGLPYTGVPLPSTFYQGPVFPVAPTSSKQHGWNVS 946
Qy 614 --TPTPPQOASGYGQHGYSYDGLDQTGTAAGDYSKGYAGSSQAPNKSAGSGPGKGV 671
Db 947 VNASATPPFQOPSGYSGHYNT-----GVS 970
Qy 672 VSSSTGLPDMTGVNKNKT-OTFDKQGFAGTPT-PPFSLPSVLGSGTGLASGAAGPYAPP 729
Db 971 VTSNTGVPIISGVSKTKQSQSEKQGFHSGTTPAASENLPSALGSGGPIPATTAAYPPA 1030
Qy 730 PFLHILPAHQPHSLHLLHLLPQDAGSGSGQSRSPSLQPKSQAASKPAYGNPYW 784
Db 1031 PFWHILTPHQPHSLHLLHLLQDGGTSGQSRQSTSSIPQKPTNKSAI-NSYSW 1084
RESULT 8
Q80X50 PRELIMINARY; PRT; 1107 AA.
AC Q80X50;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 4932431F02Rik protein.
GN Name=4932431F02Rik;

386	SSSTSH--HASVES-ASSHOSSEATSTAATSVSSASSASSGVLSSSMNTANSLCLGGTGA 442	
731	GRITSTLTLTSSVEANLHSSSTFTSTVSAPPPV-VSVSSSLNCGSSGLSLGSGN 789	
443	SSASSSSRAAPLVTSCKAPPNLPGVPLLNQYLVGPGLLPAYP--IYGYDELOMLQS 500	
790	STVTASTRSSVATTSGKAPPNLPGVPLLPNPYIMAP-GLLHAYPPQVYGYDDLOMLQT 848	
501	RLPVDYVIGPFAAPTA-LASDRSLANNPYGVDVKFGRGDSASPAPATTAPQPOQOSQ 559	
849	RFPDLYSIFPFTPTTPTLGRDGSLASNPYSGDDTKFGRGDASSAPATTAPQPOQNTQ 908	
560	THHTAQQPFWNPALPGYSYTGPLYT---GMPSAFOYGTMPF-VPPASAKOHVNL-- 613	
909	THHTTQOTFLNPALPGYSYTSPLPYTGVLPGLPSTFYGPVAFVPTSKOHGVNVSVN 968	
614	TPTPPFOQASGVGHGYSTGYDDTLTQGTAAAGDYSGKGVAGSSQAPNKSAGSGPKGVSVS 673	
969	ASATPPQQPSGYSGHYNT-----GVSVTI 992	
674	SSTTGLPDMTGSVYNTK-OTFDKQGFHAGTP-PPPSLPSVLGSTGTPLAGAAGFYAPPPF 731	
993	SSNTGVPDISGSVYKTSQGSFEKQGFHSGTAAASFNLPALSGSGRPNPATAAAYPPAPF 1052	
732	LHILPAHQPHSQLLHHLLPDAQSGSGORSQPSLOPKSOASKPAYCNGNPYW 784	
1053	MHILTPHQPHSQLLHHLLQDGQGTGSGORSOTSIPOKPTNKSAY-NSYSW 1104	

RESULT 9

Q8BJ01

ID

Q8BJ01

PRELIMINARY;

PRT; 1112 AA.

AC

Q8BJ01;

01-MAR-2003 (TREMblrel. 23, Created)

DT

01-WAR-2003 (TREMblrel. 23, Last sequence update)

DT

01-WAR-2004 (TREMblrel. 26, Last annotation update)

DE

Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone: C130046J04 product: NICE-4 PROTEIN homolog.

DE

library, clone: C130046J04 product: NICE-4 PROTEIN homolog.

GN

Name=4932431F02Rik;

OS

Mus musculus (Mouse).

OC

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX

NCBI_TaxId=10090;

OX

NCBI_TaxId=10090;

RP

SEQUENCE FROM N.A.

RC

STRAIN=C57BL/6J; TISSUE=Head;

RC

MEDLINE=99279253; PubMed=10349636;

RA

Carninci P., Hayashizaki Y.;

RA

Carninci P., Hayashizaki Y.;

RT

"High-efficiency full-length cDNA cloning.";

RL

Meth. Enzymol. 303:19-44 (1999).

RL

[1]

RP

SEQUENCE FROM N.A.

RC

STRAIN=C57BL/6J; TISSUE=Head;

RC

MEDLINE=21085660; PubMed=11217851;

RA

RIKEN FANTOM Consortium;

RT

"Functional annotation of a full-length mouse cDNA collection.";

RL

Nature 409:685-690 (2001).

RL

[3]

RP

SEQUENCE FROM N.A.

RC

STRAIN=C57BL/6J; TISSUE=Head;

RA

The FANTOM Consortium,

RA

the RIKEN Genome Exploration Research Group Phase I & II Team;

RT

"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RL

Nature 420:563-573 (2002).

RL

[4]

RP

SEQUENCE FROM N.A.

RC

STRAIN=C57BL/6J; TISSUE=Head;

RC

MEDLINE=20493374; PubMed=11042159;

RA

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA

Kanno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT

"Normalization and subtraction of cap-trapper-selected cDNAs to

[illegible]


```

Db 129 SPFSQAKLRETFGDSPTVKNLQLPSTTIENISVSVHQPOPKHIKAKRIPPASKIP 188
QY 185 ASAVEMPGADVTGLNVQGALEFGSEPSLSFGAPSENSNQIPISLYSKSLSEPLNT 244
Db 189 ASAVEMPGADVTGLNVQGALEFGSEPSLSFGAPSENSNQIPISLYSKSLSEPLNT 248
QY 245 SLSMTSAVONSTVTTSVITSCSLTSSLSNSASFPVAMSSSYDQSSVHNRIPIQSPVSSSES 304
Db 249 SLSMTSAVONSTVTTSVITSCSLTSSLSNSASFPVAMSSSYDQSSVHNRIPIQSPVSSSES 308
QY 305 APGTIMNGHGGRSQOQLD 324
Db 309 APGTIMNGHGGRSQOQLD 328

RESULT 11
AAQ89045 PRELIMINARY; PRT; 363 AA.
AC AAQ89045;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DE UPAP2.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eason D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RA "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RT Genome Res. 13:2265-2270(2003).
DR EMBL: AY358682; AAQ89045.1; -.
SQ SEQUENCE 363 AA; 38824 MW; A7B4524E0AEBD45D CRC64;

Query Match 37.9%; Score 1536; DB 2; Length 363;
Best Local Similarity 96.2%; Pred. No. 4.5e-56;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 7 SSTAVNSCS--PQSLSSVLGSGFGELAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 64
Db 9 NSVLIRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 68
QY 65 STSHPTTTTSDWLPKPTTSSQSVLSHLDFKSPQPSVLSQISQHQHOSQAVTVPBPGLE 124
Db 69 STSHPTTTTSDWLPKPTTSSQSVLSHLDFKSPQPSVLSQISQHQHOSQAVTVPBPGLE 128
QY 125 SPFSQAKLRETFGDSPTVKNLQLPSTTIENISVSVHQPOPKHIKAKRIPPASKIP 184
Db 129 SPFSQAKLRETFGDSPTVKNLQLPSTTIENISVSVHQPOPKHIKAKRIPPASKIP 188
QY 185 ASAVEMPGADVTGLNVQGALEFGSEPSLSFGAPSENSNQIPISLYSKSLSEPLNT 244
Db 189 ASAVEMPGADVTGLNVQGALEFGSEPSLSFGAPSENSNQIPISLYSKSLSEPLNT 248
QY 245 SLSMTSAVONSTVTTSVITSCSLTSSLSNSASFPVAMSSSYDQSSVHNRIPIQSPVSSSES 304
Db 249 SLSMTSAVONSTVTTSVITSCSLTSSLSNSASFPVAMSSSYDQSSVHNRIPIQSPVSSSES 308
QY 305 APGTIMNGHGGRSQOQLD 324

```

```

Db 309 APGTIMNGHGGRSQOQLD 328
QY 305 APGTIMNGHGGRSQOQLD 328

RESULT 12
Q8CIG7 PRELIMINARY; PRT; 1067 AA.
AC Q8CIG7;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Nice-4 protein homolog, isoform 2.
GN Name=4932431F02Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ugin T.B., Toshitoki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzyzinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL: BC023906; AAH23906.1; -.
DR MGI:1921633; 4932431F02Rik.
DR InterPro; IPR000449; UBA_like.
DR InterPro; IPR009060; UBA_1.
DR Pfam; PF00627; UBA; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS50030; UBA; 1.
SQ SEQUENCE 1067 AA; 112451 MW; FBE932FB2D4DBB6F CRC64;

Query Match 37.5%; Score 1520; DB 2; Length 1067;
Best Local Similarity 45.2%; Pred. No. 6.3e-55;
Matches 363; Conservative 109; Mismatches 207; Indels 124; Gaps 29;

QY 3 PGTSSTAVNSCS--PQSLSSVLGSGFGELAPPKMANITSSQILDQK-APSLGQFTTTPST 61
Db 327 PASGS-----TFHHHSMVSMGLKGFVDGVEAKSGSTGQFLEQFKTAQALAA---- 377
QY 62 QONSTSHPTTTTSDWLPKPTTSSQSVLSHLDFKSPQPSVLSQISQHQHOSQAVTVPBPGLE 109
Db 378 -QHSQSGSTTTSSWDM--GSTTQSPSLVQYDLKSAND-STVHSPFTKRAFTTSSMTMEVF 434
QY 110 -QHSQAV-----TVPPGLESPFSQAKLRETFGDSPTVKNLQLPSTTIENISVSVHQ 164
Db 435 LQSPKPAVATSTAAPPPSPSPFSKS---TSAQMSFGSSDNGSSSF-----Q 479
QY 165 PQPKHIKAKRIPPASKIPASAVEMPGADVTGLNVQGALEFGSEPSLSFGAP-SS 223

```


db 1053 MHILTPHQPPHSQILHHHLQQDGG 1076

050101114
1 9 5 7 0

ON Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN SOURCE FROM N.A.
 pp

MEDLINE=2288257; PubMed=12477932;
 Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T.I., Wang J., Hsieh F.,
 Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Sheeetz T.E.,
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J.J., Abramson R.D., Mullaly S.J.,
 Bask A.S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J.J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [2]

RA Strausberg R. (May-2001) to the EMBL/GenBank/DBJ databases.
RL Submitted (RA-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC007890; AAH07890.1; -.
FT non ter 1
CO sequence 263 AA: 469DAF3ABEFDDE41 CRC64;

Query Match	35.3%	Score 1433;	DB 2;	Length 263;
Best Local Similarity	100.0%	Pred. No. 5.6e-52;		
Matches 263;	Conservative	0;	Mismatches 0;	Indels 0;
	Gaps	0;		

	Qy	524	LANNPYGDVTKFGRGDSASPAATTTPAQPOOSQSTHTTAQQPFVNPAUFPFGISLGLP	368
	Dd	1	LANNPYGDVTKFGRGDSASPAATTTPAQPOOSQSTHTTAQQPFVNPAUFPFGISYTGLP	60

DQ		GYSKGGYAGSSQAAPNKSAGSGPGKGVSSTTGLPDMTGVSYNKTQTFDKQGFGHAGTP	703
QY	644	GYSKGGYAGSSQAAPNKSAGSGPGKGVSSTTGLPDMTGVSYNKTQTFDKQGFGHAGTP	703
DB	121	GYSKGGYAGSSQAAPNKSAGSGPGKGVSSTTGLPDMTGVSYNKTQTFDKQGFGHAGTP	180
QY	704	PPPSLPSVLGSGTGPLASGAAPGYAPPPFHHILPAHQPHSQQLIHHLHPDAQSGGSQRQ	763
DB	181	PPPSLPSVLGSGTGPLASGAAPGYAPPPFHHILPAHQPHSQQLIHHLHPDAQSGGSQRQ	240

Qy 764 PSSLOPKSOASKPAYGNSPYWTN 786
Db 241 PSSLOPKSOASKPAYGNSPYWTN 263

Search completed: January 31, 2005, 17:47:01
Job time : 210 secs

This Page Blank (uspto)